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From: Jiang, Dong
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Priority: 8/14/99
Chen (Genetech)

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-commercial

no art.

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).
Thank you very much.

Dong Jiang (78243)
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U.S. Patent and Trademark Office
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TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:49 ; Search time 29.85 Seconds
(without alignments)
733.050 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLPLGLFLTLWHTCLAHH.....FHTFTHVPVGTCVLPFRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	21	AA18911 A novel polypeptid
2	1073	100.0	197	21	AA18911 A human interleuki
3	1073	100.0	197	21	AA18911 A human interleuki
4	1073	100.0	197	21	AA18911 Human interleukin-
5	1073	100.0	197	21	AA18911 Human interleukin-
6	1073	100.0	197	21	AA18911 Amino acid sequenc
7	1073	100.0	197	21	AA18911 Human interleukin
8	1073	100.0	197	22	AA18911 Human PRO polypept
9	1073	100.0	197	22	AA18911 Human interleukin
10	1073	100.0	206	21	AA18911 Human Interleukin
11	1073	100.0	425	21	AA18911 Human Interleukin

12	1063	99.1	227	22	AAE08676	Human interleukin
13	1061	98.9	227	22	AAE08680	Human interleukin
14	1061	98.9	227	22	AAE08682	Human interleukin
15	1060	98.8	227	22	AAE08681	Human interleukin
16	1060	98.8	227	22	AAE08685	Human interleukin
17	1059	98.7	227	22	AAE08684	Human interleukin
18	1059	98.7	227	22	AAE08687	Human interleukin
19	1058	98.6	227	22	AAE08679	Human interleukin
20	1058	98.6	227	22	AAE08683	Human interleukin
21	1058	98.6	227	22	AAE08686	Human interleukin
22	1055	98.3	227	22	AAE08690	Human interleukin
23	1054	98.2	227	22	AAE08688	Human interleukin
24	1054	98.2	227	22	AAE08689	Human interleukin
25	1054	98.2	227	22	AAE08691	Human interleukin
26	1054	98.2	227	22	AAE08693	Human interleukin
27	1054	98.2	227	22	AAE08695	Human interleukin
28	1054	98.2	227	22	AAE08697	Human interleukin
29	1054	98.2	227	22	AAE08699	Human interleukin
30	1054	98.2	227	22	AAE08701	Human interleukin
31	1054	98.2	227	22	AAE08703	Human interleukin
32	1053	98.1	227	22	AAE08692	Human interleukin
33	1053	98.1	227	22	AAE08694	Human interleukin
34	1053	98.1	227	22	AAE08696	Human interleukin
35	1053	98.1	227	22	AAE08698	Human interleukin
36	1053	98.1	227	22	AAE08700	Human interleukin
37	1053	98.1	227	22	AAE08702	Human interleukin
38	1034	96.4	223	22	AAE08677	Human mature inter
39	459	42.8	87	21	AA153890	Partial amino acid
40	459	42.8	87	21	AA153890	Human interleukin
41	446	41.6	123	21	AA153890	A human interleuki
42	446	41.6	123	21	AA153890	A human interleuki
43	199	18.5	202	21	AA153890	A human interleuki
44	199	18.5	202	21	AA153890	A human interleuki
45	199	18.5	202	21	AA153890	Human transforming

ALIGNMENTS

RESULT 1	
AA18911	AA18911 standard; Protein; 197 AA.
ID	AA18911 standard; Protein; 197 AA.
XX	
AC	AA18911;
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	A novel polypeptide designated PRO1122.
XX	
KW	Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW	PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW	PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW	PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW	insulinemia; kidney disorder; Bergers disease; nephropathy;
KW	Schonelein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW	Crohn's disease.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..18
FT	/note= "signal peptide"
FT	3..25
FT	/note= "leucine zipper pattern"
FT	32..38
FT	/note= "N-myristoylation site"
FT	55..61
FT	/note= "N-myristoylation site"
FT	112..121
FT	/note= "tyrosine kinase phosphorylation site"
FT	133..139
XX	
PN	WO200056889-A2.

XX 28-SEP-2000.
PD
XX
PF
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
PR 23-MAR-1999; 99US-0125774.
PR 23-MAR-1999; 99US-0125778.
PR 24-MAR-1999; 99US-0125826.
PR 31-MAR-1999; 99US-0127035.
PR 05-APR-1999; 99US-0127706.
PR 21-APR-1999; 99US-0130359.
PR 27-APR-1999; 99US-0131270.
PR 27-APR-1999; 99US-0131272.
PR 27-APR-1999; 99US-0131291.
PR 04-MAY-1999; 99US-0132371.
PR 04-MAY-1999; 99US-0132379.
PR 04-MAY-1999; 99US-0132383.
PR 25-MAY-1999; 99US-0135750.
PR 08-JUN-1999; 99US-0138166.
PR 20-JUL-1999; 99US-0144791.
PR 03-AUG-1999; 99US-0146970.
PR 09-DEC-1999; 99US-0170262.
XX
PA (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WL, Zhang Z;
PI
XX
DR WPI: 2000-628263/60.
DR N-PSDB; AAA96338.
XX
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use -
XX
XX Claim 12; Fig 6; 222pp; English.
XX
XX The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger's disease or other
CC nephropathies associated with Schönlein-Henoch purpura, celliac disease,
CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLELTWLTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtlplglflftwltclahhdpslrghshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHQRSISPRYRVDTDEDRY 120
DB 61 alpvalvssleashrgrherpsattqcpvlrpeevleadthqrsispryrvdtde dry 120
QY 121 POKLAFAECLRCGICDARTGRETAAALNSVRLQLSLVLRPPCSRDGSLPTPGAFAFHT 180
DB 121 pqlafaeclrcgicdartgretaalnsvrlqlslvlrrppcsrdgslptpgafafht 180

QY 181 EFTHVPVGCTCVLPRSV 197
DB 181 efthvpvgctcvlprsv 197
RESULT 2
AAB07602
ID AAB07602 standard; Protein; 197 AA.
XX
AC AAB07602;
XX
DT 07-NOV-2000 (first entry)
XX
DE A human interleukin (IL) 171 polypeptide.
XX
KW Interleukin: IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW IL-177; IL-171; cell proliferation; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /note= "signal peptide"
FT Protein 18..197
FT /note= "mature protein"
XX
PN WO200042188-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00006.
XX
PR 11-JAN-1999; 99US-0228822.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM, Bazan JF, Kastelein RA;
XX
DR WPI: 2000-466130/40.
DR N-PSDB; AAA58991.
XX
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like
PT protein used to identify genes for homologous proteins -
XX
XX Disclosure; Page 20-21; 111pp; English.
XX
CC The present sequence represents an interleukin-171 (IL-171) polypeptide.
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
CC member of a new group of interleukins, IL-170 polypeptides. The members
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
CC protein can be used to treat abnormal proliferation e.g. cancer
CC or degenerative conditions. Antibodies can be used in diagnostic
CC methods to detect over production of IL-170 protein in cells or body
CC fluids.
XX
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLELTWLTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtlplglflftwltclahhdpslrghshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHQRSISPRYRVDTDEDRY 120
DB 61 alpvalvssleashrgrherpsattqcpvlrpeevleadthqrsispryrvdtde dry 120
QY 121 POKLAFAECLRCGICDARTGRETAAALNSVRLQLSLVLRPPCSRDGSLPTPGAFAFHT 180
DB 121 pqlafaeclrcgicdartgretaalnsvrlqlslvlrrppcsrdgslptpgafafht 180

Db	121	pqlafaeclrcgcidartgretaaalnsvllqslvlvrrrrpcsdrgslptpgafafht	180
QY	181	EFIHVPVGCTCVLPRSV 197	
Db	181	efihvpvgctcvlprsv 197	
RESULT 3			
ID	AA07684		
XX	AA07684	standard; Protein; 197 AA.	
AC	AA07684;		
XX			
DT	07-NOV-2000	(first entry)	
XX			
DE	A human interleukin-171 polypeptide.		
XX			
KW	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;		
KW	IL-174; IL-176; IL-177; cell proliferation; cancer.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT		/note= "signal peptide"	
FT	Protein	18..197	
FT		/note= "mature protein"	
FT	Modified-site	55..57	
FT		/note= "putative glycosylation site"	
XX			
PN	WO200042187-A1.		
XX			
PD	20-JUL-2000.		
XX			
PF	10-JAN-2000; 2000WO-US000005.		
XX			
PR	11-JAN-1999; 99US-0229402.		
XX			
PA	(SCHE) SCHERING CORP.		
PI	Gorman DM, Bazan JF, Kastelein RA;		
XX			
DR	WPI; 2000-476060/41.		
DR	N-PSDB; AAA59149.		
XX			
PT	New DNA sequence encoding a mammalian homolog of CTLA-8, designated		
PT	interleukin-171 (IL-171), useful for recombinant production of IL-171		
PT	which can be used for treating conditions associated with abnormal		
PT	physiology or development -		
XX			
PS	Claim 11; Page 10-11; 11lpp; English.		
XX			
CC	The present sequence represents an interleukin (IL)-171 polypeptide.		
CC	It is a mammalian homologue of the cytokine designated CTLA-8 (also		
CC	referred to as IL-17). The specification also describes homologues		
CC	IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA		
CC	sequence encoding IL-171 is useful for identifying genes, mRNA and		
CC	cDNA molecules which code for related or homologous proteins. The		
CC	IL-171 protein, antibodies against IL-171, and compounds which have		
CC	binding affinity to IL-171 are useful in treatment of conditions		
CC	associated with abnormal physiology or development, including abnormal		
CC	proliferation, e.g. cancerous conditions, or degenerative conditions.		
CC	The IL-171 protein can be used in kits and assay methods for identifying		
CC	compounds that selectively bind to IL-171.		
XX			
SQ	Sequence 197 AA;		
Query Match 100.0%; Score 1073; DB 21; Length 197;			
Best Local Similarity 100.0%; Pred. No. 4.6e-109;			
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	mtlpgllfltwlhtclahdpsslrghpshgtphcysaeelpgqapphllargakwq	60
QY	61	ALPVALVSSLEAASHRHRRPSATTQCPLVRPEEVLADTHORSISPWRYRVDTDDEY	120
Db	61	alpvalvssleaashrgrherpsattqcplvrpeeveadthrsispswryrvdtdey	120
QY	121	PKLAFAECLRCGCIDARTGRETAAALNSVRLQLSLVLRRRPCSRDGLPTPGAFAFHT	180
Db	121	pqlafaeclrcgcidartgretaaalnsvllqslvlvrrrrpcsdrgslptpgafafht	180
QY	181	EFIHVPVGCTCVLPRSV 197	
Db	181	efihvpvgctcvlprsv 197	
RESULT 4			
AA	Y92238		
ID	AA92238	standard; Protein; 197 AA.	
XX			
AC	AA92238;		
XX			
DT	10-AUG-2000	(first entry)	
XX			
DE	Human interleukin-17 (IL-17) homologue.		
XX			
KW	Interleukin 17; IL-17; haematopoiesis; chemotherapy; cytostatic;		
KW	antianemic; cardiant; hemostatic; anti-inflammatory; anti-HIV.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..18	
FT		/label= signal_peptide	
FT	Protein	19..197	
FT		/label= mature_protein	
XX			
PN	WO200020593-A1.		
XX			
PD	13-APR-2000.		
XX			
PF	30-SEP-1999; 99WO-US22678.		
XX			
PR	02-OCT-1998; 98US-0102883.		
PR	01-DEC-1998; 98US-0110405.		
PR	11-JUN-1999; 99US-0138910.		
XX			
PA	(ELIL) LILLY & CO ELI.		
XX			
PI	Glasebrook AL, Su EW, Wei J, Liu L;		
XX			
DR	WPI; 2000-303778/26.		
DR	N-PSDB; AAA09153.		
XX			
PT	Nucleic acid encoding an interleukin-17 (IL-17) homolog polypeptide		
PT	which enhances hematopoiesis, useful for treating e.g. anemia,		
PT	thrombocytopenia, viral and bacterial infections		
XX			
PS	Claim 16; Page 92-93; 11lpp; English.		
XX			
CC	Interleukin 17 (IL-17) stimulates hematopoiesis and production of		
CC	neutrophils, granulocytes, or platelets, this may be useful during		
CC	chemotherapy. IL-17 homologues have at least one activity selected		
CC	from induction of cytotoxic T cells, induction of lymphokine-activated		
CC	killer cell proliferation or a B or T cell stimulation. The IL-17		
CC	homologue may also be used to treat viral or bacterial infections,		
CC	immune related diseases, anemia, leukemia, thrombocytopenia, uremia,		
CC	Von Willebrand disease, postoperative cardiovascular dysfunction,		
CC	treatment of AIDS (acquired immune deficiency syndrome)-related bone		
CC	marrow failure, and inflammatory diseases of the gastrointestinal		
CC	system, joints, and lungs.		
XX			
SQ	Sequence 197 AA;		

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPPLLARGAKWGQ 60
DB 1 mtlplgllflitwhltclahhdpslrghphshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGHERPSATTQCPVLRPEEVLEADTHORSISPWRYRVDTDDEY 120
DB 61 alpvalvssleashaashrgherpsattqcpvlrpeevleadthgrsispwryrvdtddedry 120
QY 121 PQLAFACELCRGICDARTGRETAAALNSVRLQLSLVLRPPCSRDCGSLPTPCAFAFHT 180
DB 121 pqlafaecelcrgicdartzetaalnsrvllqslvlrrrpscdsgslptpgafafht 180
QY 181 EFHVPVGCCTCVLPRSV 197
DB 181 efihvpvgctcvlprsv 197

RESULT 5
AA44460
ID AAY44460 standard; Protein; 197 AA.
XX AAY44460;
AC
XX
DT 27-MAR-2000 (first entry)
XX Human Interleukin 17C, PRO1122 polypeptide.
KW Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UN0561;
KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;
KW hybridisation probe; antagonist; degenerative cartilaginous disorder;
KW agonist; diagnosis; therapy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein 19..197 /label= Signal_peptide
FT /label= Mature_IL-17C_polypeptide
FT /note= "Used to treat degenerative cartilaginous disorder"
FT Misc-difference 109 /note= "Conserved Trp residue"
FT Misc-difference 129 /note= "Conserved Cys residue"
FT Misc-difference 134 /note= "Conserved Cys residue"
FT Misc-difference 163 /note= "Conserved Cys residue"
FT Misc-difference 189 /note= "Conserved Cys residue"
FT Misc-difference 191 /note= "Conserved Cys residue"
XX WO960127-A2.
XX
XX 25-NOV-1999.
XX 14-MAY-1999; 99WO-US10733.
XX
PR 15-MAY-1998; 98US-0085579.
PR 23-DEC-1998; 98US-0113621.
XX
XX (GETH) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;

DR WPI; 2000-116314/10.
XX N-PSDB; AAZ29728.
PT New polypeptides designated PRO1031 and PRO1122 used to treat a
PT degenerative cartilaginous disorder -
XX Claim 23; Fig 3; 14lpp; English.
PS
XX The present sequence is the human PRO1122 polypeptide, also referred to
CC as UN0561, and as interleukin-17C (IL-17C), encoded by
CC clone DNA62377-1381-1. This sequence has identity with the
CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
CC and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
CC intestine, stomach and testis also. It shares about 26-28% amino acid
CC identity with IL-17 and IL-17B. The entire coding region of IL-17C can
CC be used as hybridisation probe. The PRO1122 polypeptide, agonist or
CC antagonist, is used to diagnose and treat a degenerative cartilaginous
CC disorder.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPPLLARGAKWGQ 60
DB 1 mtlplgllflitwhltclahhdpslrghphshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGHERPSATTQCPVLRPEEVLEADTHORSISPWRYRVDTDDEY 120
DB 61 alpvalvssleashaashrgherpsattqcpvlrpeevleadthgrsispwryrvdtddedry 120
QY 121 PQLAFACELCRGICDARTGRETAAALNSVRLQLSLVLRPPCSRDCGSLPTPCAFAFHT 180
DB 121 pqlafaecelcrgicdartzetaalnsrvllqslvlrrrpscdsgslptpgafafht 180
QY 181 EFHVPVGCCTCVLPRSV 197
DB 181 efihvpvgctcvlprsv 197

RESULT 6
AAY53892
ID AAY53892 standard; Protein; 197 AA.
XX AAY53892;
AC
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of human interleukin-21.
XX
KW Human; interleukin-22; IL-22; IL-21; immune system disorder;
KW Immune cell chemotaxis; haematopoietic cell disorder;
KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;
KW inflammation; hyperproliferative disorder; tissue regeneration;
KW embryonic stem cell differentiation; embryonic stem cell proliferation;
KW haematopoietic lineage; allergic asthma.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..18 /note= "Signal peptide"
FT Domain 34..40 /note= "Conserved domain V"
FT Domain 63..68 /note= "Conserved domain VI"
FT Domain 104..109 /note= "Conserved domain VII"
FT Domain 113..121

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FT          /note= "conserved domain I"
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FT          156..162
FT          /note= "conserved domain III"
FT          185..192
FT          /note= "conserved domain IV"
XX
XX WO9961617-AL.
PN
XX
XX PD 02-DEC-1999.
XX
XX PF 27-MAY-1999; 99WO-US11644..
XX
XX PR 29-MAY-1998; 98US-0087340.
XX PR 10-SEP-1998; 98US-0099805.
XX PR 30-APR-1999; 98US-0131965.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Ruben SM, Ebner R;
XX
XX WPI; 2000-072622/06.
XX N-PSDB; AAZ36836.
XX
XX Novel polynucleotides used to develop products for treating e.g. immune
XX disorders, blood disorders, autoimmune disorders, allergies,
XX inflammation, hyperproliferative disorders or infections -
XX
XX Claim 26; Fig 6A-B; 170pp; English.
XX
XX The present sequence represents a human interleukin-21 (IL-21)
XX protein. The specification also describes IL-22 polynucleotides and
XX polypeptides. The IL-21 polynucleotide was isolated from a cDNA library
XX of apoptotic T-cells. IL-21 and IL-22 may be useful in treating
XX deficiencies or disorders of the immune system, by activating or
XX inhibiting the proliferation, differentiation, or mobilization
XX (chemotaxis) of immune cells, treating or detecting deficiencies or
XX disorders of haematopoietic cells, to modulate haemostatic or
XX thrombolytic activity, in treating or detecting autoimmune disorders,
XX treating asthma (particularly allergic asthma) or other respiratory
XX problems, to treat and/or prevent organ rejection or graft-versus-host
XX disease (GVHD), to modulate inflammation, to treat or detect
XX hyperproliferative disorders, to treat or detect infectious agents, to
XX differentiate, proliferate and attract cells, leading to the
XX regeneration of tissues, IL-21 and IL-22 may also increase or decrease
XX the differentiation or proliferation of embryonic stem cells and
XX haematopoietic lineage, may be used to modulate mammalian
XX characteristics.
XX
XX SQ Sequence 197 AA;
Query Match 100.08; Score 1073; DB 21; Length 197;
Best Local Similarity 100.08; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTLPLGLFLTLWHLTCLAHHDPSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
Db 1 mtlpgllfltlwhtclahhdpslrgphshgtphcysaeelpgqapphllargakwgq 60
QY 61 ALPVALVSSLEASHRGHERPSATTQCPLRPEEVLEADTHQRSTSPWRYRVDTDEDRY 120
Db 61 alpvalvssleashrgherpsattqcpvlrpeevleadthqrsispwryrvdtdedry 120
QY 121 POKLFAECLRCGCDIDARTGRTAALNSVRLQLSLVLRRCSDRGSLPPGAFVHT 180
Db 121 pklfaeclrcgcdcldartgrtaalnsvrlqlslvlrrrcsdrsgslptpgafafht 180
QY 181 EFHVPVGCCTCVLPVRSV 197
Db 181 efihvpvgctcvlprsv 197
```

```
RESULT 7
AAG66121
ID AAG66121 standard; Protein; 197 AA.
XX
XX AC AAG66121;
XX
XX DT 13-MAR-2002 (first entry)
XX
XX DE Human Interleukin (IL)-21 amino acid sequence.
XX
XX KW Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;
XX antiinflammatory; antibacterial; gene therapy; human.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT Peptide
XX FT /note= "signal peptide"
XX FT Protein
XX FT /note= "mature protein"
XX FT Domain
XX FT /note= "conserved domain V"
XX FT Domain
XX FT /note= "conserved domain VI"
XX FT Domain
XX FT /note= "conserved domain VII"
XX FT Domain
XX FT /note= "conserved domain I"
XX FT Domain
XX FT /note= "conserved domain II"
XX FT Domain
XX FT /note= "conserved domain III"
XX FT Domain
XX FT /note= "conserved domain IV"
XX
XX US2001023070-A1.
XX 20-SEP-2001.
XX
XX 08-DEC-2000; 2000US-0731816.
XX
XX 29-MAY-1998; 98US-087340P.
XX 30-APR-1999; 99US-131965P.
XX 09-DEC-1999; 99US-169837P.
XX 27-MAY-1999; 99US-0320713.
XX 27-MAY-1999; 99WO-US11644.
XX
XX (EBNE/) EBNER R.
XX (RUBE/) RUBEN S M.
XX
XX Ebner R, Ruben SM;
XX
XX WPI; 2001-638470/73.
XX N-PSDB; AAL67878.
XX
XX New interleukin-21 and interleukin-22 polynucleotides and polypeptides,
XX useful for treating, preventing or diagnosing e.g. disorders of
XX hematopoietic cells, autoimmune disorders, or hyperproliferative
XX diseases -
XX
XX Claim 26; Fig 6A-B; 87pp; English.
XX
XX The invention relates to novel human proteins designated interleukin
XX (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in
XX linkage analysis as a marker for those specific chromosome, in chromosome
XX mapping, to control gene expression through triple helix formation or
XX antisense DNA or RNA, in gene therapy, in identifying individuals from
XX minute biological samples, as an alternative to restriction fragment
XX length polymorphism (RFLP) analysis, as polymorphic markers for forensic
XX purposes, as molecular weight markers, or as diagnostic probes. IL-21 and
XX IL-22 polypeptides can be used to treat, prevent or diagnose diseases of
XX the immune system by activating or inhibiting the proliferation,
```

CC differentiation or mobilization of immune cells, disorders of
CC hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV)
CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's
CC disease, systemic lupus erythematosus, ophthalmia), graft versus host
CC disease, inflammation, hyperproliferative disorders, or infectious
CC diseases. The polypeptides are useful for generating antibodies, which
CC can be used to treat, inhibit or prevent diseases or conditions
CC associated with aberrant expression and/or activity of IL-21 or IL-22.
CC The present sequence represents the amino acid sequence of human IL-21.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSABEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtllpgllflftwlhtclahhdpslrghphshgtphcysaeelpgqapphllargakwgq 60
QY 61 ALPALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPWRYRVDTDedry 120
DB 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrsispwryrvdtdedry 120
QY 121 POKLAFACELRCGICDARTGRETAALNSVRLQLSLVLRPPCRSDGSLPTGCAFAFHT 180
DB 121 pqklafaeclrcgcidartgreetaalnsrvllqslvlrrppcsrdgslptpgafafht 180
QY 181 EFTHPVGCVCVLPVRSV 197
DB 181 eflhvpvgctcvlprsv 197

RESULT 8
AAU29247
ID AAU29247 standard; Protein; 197 AA.
XX
AC AAU29247;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #224.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.

XX
PR 01-MAR-2000; 2000WO-US03601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-064848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
(GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS46148.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
XX Claim 11; Fig 448; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSABEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtllpgllflftwlhtclahhdpslrghphshgtphcysaeelpgqapphllargakwgq 60
QY 61 ALPALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPWRYRVDTDedry 120
DB 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrsispwryrvdtdedry 120
QY 121 POKLAFACELRCGICDARTGRETAALNSVRLQLSLVLRPPCRSDGSLPTGCAFAFHT 180
DB 121 pqklafaeclrcgcidartgreetaalnsrvllqslvlrrppcsrdgslptpgafafht 180

QY 181 EFIHVPVGTCTVLPKRSV 197
 PT |||||||
 Db 181 efihvpvgctcvlprsv 197

RESULT 9

AAU04951
 ID AAU04951 standard; Protein; 197 AA.

XX AC AAU04951;

DT 24-OCT-2001 (first entry)

XX DE Human Interleukin 17C ligand, IL-17C.

XX KW Human; Interleukin-17C ligand; IL-17C; agonist; antagonist;
 KW PRO1122; DNA 62377-1381-1; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KW allergic disease; asthma; demyelinating disease;
 KW degenerative cartilaginous disorder; transplantation associated disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..18

FT /label= Signal_peptide

FT Region 3..25

FT /note= "Leucine zipper pattern"

FT Protein 19..197

FT /label= Mature_IL_17C

FT Region 32..38

FT /note= "N-myristoylation site"

FT Region 55..61

FT /note= "N-myristoylation site"

FT Region 99..125

FT /note= "Region homologous to IL-17"

FT Region 112..121

FT /note= "Tyrosine kinase phosphorylation site"

FT Region 133..139

FT /note= "N-myristoylation site"

XX WO200146420-A2.

XX PD 28-JUN-2001.

XX PF 20-DEC-2000; 2000WO-US34956.

XX PR 23-DEC-1999; 99US-0172096.

XX PR 30-DEC-1999; 99WO-US31274.

XX PR 11-JAN-2000; 2000US-0175481.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 02-MAR-2000; 2000WO-US05841.

XX PR 21-MAR-2000; 2000US-0191007.

XX PR 21-MAR-2000; 2000WO-US07532.

XX PR 02-JUN-2000; 2000WO-US15264.

XX PR 22-JUN-2000; 2000US-0213087.

XX PR 24-AUG-2000; 2000US-0644848.

XX PR 24-AUG-2000; 2000WO-US23328.

XX PR 24-OCT-2000; 2000US-0242837.

XX PR 10-NOV-2000; 2000WO-US30873.

XX PR 28-NOV-2000; 2000US-0253646.

XX PR 01-DEC-2000; 2000WO-US32678.

XX (GETH) GENENTECH INC.

XX PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL;

PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

XX WPI; 2001-451708/48.

XX DR N-PSDB; AAS09510.

XX

PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 PT arthritis and diabetes -

XX PS Claim 10; Fig 4; 188pp; English.

XX CC The sequence is PRO1122 which is the human Interleukin 17C ligand,
 CC IL-17C, encoded by DNA 62377-1381-1. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food
 CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polyneuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLETLWLHTCLAHDPFSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60

Db 1 mtlplgllfltlwhtclahdpfslrgphshgtphcysaeelpgqapphllargakwgq 60

QY 61 ALPVALVSSLEAASHRGHRERPSATTCQPVLRPEEVLEADTHORSISPRYRVDTDEDRY 120

Db 61 alpvalvssleashrgrhrerpsattcqpvlrpeevleadthqrsispryrvdtdedry 120

QY 121 POKLFAECLRCGIDARTGRTAALNSVRLQLSLVLRRCRDSGLPTPGAFAFHT 180

Db 121 pqklfaeclrcgicdartgretaalnsvrlqlslvllrrpcsdrgsglptpgafafht 180

QY 181 EFIHVPVGTCTVLPKRSV 197

Db 181 efihvpvgctcvlprsv 197

RESULT 10

AAU44485

ID AAY44485 standard; Protein; 206 AA.

XX AC AAY44485;

XX DT 27-MAR-2000 (first entry)

XX DE Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.

XX KW Interleukin; IL-17C.his; PRO1122 polypeptide; clone DNA62377-1381-1;
 KW immunoprecipitation; IL-17 receptor extracellular domain; IL-17R ECD;
 KW cytokine IL-17; hybridisation probe; antagonist; Gly(His)8 tag; agonist;
 KW degenerative cartilaginous disorder; diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..18

FT /label= Signal_peptide

FT Protein 19..197

FT /label= Mature_IL-17C.polypeptide

FT /note= "Used to treat degenerative cartilaginous
 disorder"

FT Misc-difference 109

FT /note= "Conserved Trp residue"

```
FT Misc-difference 129 /note= "Conserved Cys residue"
FT Misc-difference 134 /note= "Conserved Cys residue"
FT Misc-difference 163 /note= "Conserved Cys residue"
FT Misc-difference 189 /note= "Conserved Cys residue"
FT Misc-difference 191 /note= "Conserved Cys residue"
FT Misc-difference 198..206 /note= "C-terminal Gly(His)8 tag"
XX
XX WO9960127-A2.
XX
XX 25-NOV-1999.
XX
XX 14-MAY-1999; 99WO-US10733.
XX
XX 15-MAY-1998; 98US-0085579.
XX 23-DEC-1998; 98US-0113621.
XX
XX (GETH ) GENENTECH INC..
XX
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;
XX
XX WPI; 2000-116314/10.
XX
XX New polypeptides designated PRO1031 and PRO1122 used to treat a
XX degenerative cartilaginous disorder -
XX
XX Example 11; Page 138-139; 141pp; English.
XX
XX The present sequence is the human PRO1122 polypeptide, with a C-terminal
XX Gly(His)8 tag, IL-17C.his, derived from the clone DNA62377-1381-1.
XX This sequence is used in a competitive binding experiment for the
XX immunoprecipitation of IL-17 receptor extracellular domain (IL-17R ECD).
XX The entire coding region of IL-17C can be used as hybridisation probe.
XX The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and
XX treat a degenerative cartilaginous disorder.
XX
XX Sequence 206 AA;

Query Match 100.0%; Score 1073; DB 21; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGOAPPHLLARGAKWGQ 60
Db 1 mtlplgllftwlhtclahhdpslrghpshgtphcsaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRHERPSATTQCPVLRPEEVEADTHQRSISPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeeveadthgrsispwryrvdtde 120
QY 121 POKLAFAECLRCGIDARTGRETAAALNSVRLQSLVLRRRRCSRDSGLPTPGAFAFHT 180
Db 121 pqlafaeclrcgidartgretaaalnsvrlqslvlrrrrpcsrdsrglptpgafafht 180
QY 181 EFTHVPVGCVCVLPVRSV 197
Db 181 efthvpvgctcvlprsv 197

RESULT 11
AAY44462
ID AAY44462 standard; Protein; 425 AA.
XX
XX AAY44462;
XX
XX 27-MAR-2000 (first entry)
XX
```

```
DE Human Interleukin 17C-IgG1 Fc fusion protein, hIL-17C.fc.
XX
XX Interleukin; IL-17C.fc; fusion protein; PRO1122 polypeptide; cytokine;
XX human IgG1; fluorescence-activated cell sorter analysis; FACS;
KW Tumour Necrosis Factor-alpha; TNF-alpha; leukemic monocyte; THP-1 cell.
XX
XX Homo sapiens.
XX
XX Key
XX Peptide
XX 1..18
XX /label= Signal_peptide
XX 19..197
XX /label= Mature_IL-17C-polypeptide
XX /note= "Used to treat degenerative cartilaginous
XX disorder"
XX
XX Misc-difference 109 /note= "Conserved Trp residue"
XX
XX Misc-difference 129 /note= "Conserved Cys residue"
XX
XX Misc-difference 134 /note= "Conserved Cys residue"
XX
XX Misc-difference 163 /note= "Conserved Cys residue"
XX
XX Misc-difference 189 /note= "Conserved Cys residue"
XX
XX Misc-difference 191 /note= "Conserved Cys residue"
XX 197..425
XX /note= "Sequence derived from Fc region of human IgG1"
XX
XX WO9960127-A2.
XX
XX 25-NOV-1999.
XX
XX 14-MAY-1999; 99WO-US10733.
XX
XX 15-MAY-1998; 98US-0085579.
XX 23-DEC-1998; 98US-0113621.
XX
XX (GETH ) GENENTECH INC..
XX
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;
XX
XX WPI; 2000-116314/10.
XX
XX New polypeptides designated PRO1031 and PRO1122 used to treat a
XX degenerative cartilaginous disorder -
XX
XX Example 12; Page 129-130; 141pp; English.
XX
XX The present sequence is the human IL-17C.fc fusion protein, derived from
XX PRO1122 polypeptide and the Fc region of human IgG1. The cytokine IL-17C
XX can be used to induce the release of TNF-alpha from human leukemic
XX monocytic, THP-1 cells. The fusion protein, IL-17C.fc is used to identify
XX the binding of IL-17C to THP-1 cells, using fluorescence-activated cell
XX sorter analysis (FACS).
XX
XX Sequence 425 AA;

Query Match 100.0%; Score 1073; DB 21; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGOAPPHLLARGAKWGQ 60
Db 1 mtlplgllftwlhtclahhdpslrghpshgtphcsaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRHERPSATTQCPVLRPEEVEADTHQRSISPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeeveadthgrsispwryrvdtde 120
QY 121 POKLAFAECLRCGIDARTGRETAAALNSVRLQSLVLRRRRCSRDSGLPTPGAFAFHT 180
```

Db 121 pqlklfaeclrgcdartgretalnsrvllqslvllrrpcsrdsqslptpgafafht 180
 Qy 181 EFHVPVGGCTCVLPVRSV 197
 Db 181 efihvpvgctcvlprsv 197

RESULT 12
 AAE08676
 ID AAE08676 standard; Protein; 227 AA.
 AC AAE08676;
 XX 15-NOV-2001 (first entry)
 DT Human interleukin (IL)-17 like protein.
 DE
 XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
 KW multiple sclerosis; graft versus host disease; inflammatory disease;
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
 KW neuroprotective; antirheumatic; antiallergic.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 5..48
 FT /label= Signal_peptide
 FT Protein 49..227
 FT /label= Mature_human_IL-17_like protein
 XX
 PN WO200159120-A2.
 XX 16-AUG-2001.
 XX
 PF 07-FEB-2001; 2001WO-US03916.
 XX
 PR 08-FEB-2000; 2000US-0180864.
 XX 27-NOV-2000; 2000US-0722920.
 PR (AMGE-) AMGEN INC.
 XX
 PI Jing S, Bass MB;
 XX WPI; 2001-529841/58.
 DR N-PSDB; AAD15291.
 XX
 PT Novel interleukin-17 like polypeptides and nucleic acid molecules
 PT encoding them useful for diagnosis, prevention and treatment of
 PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
 PT rejection
 XX
 PS Claim 14; Fig 1A; 117pp; English.

The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in

CC gene therapy and for mapping the location of the IL-17 like gene and
 CC related genes on chromosomes, as hybridisation probes in diagnostic
 CC assays. Non-human animals in which the promoter for one or more of IL-17
 CC like protein is either activated or inactivated are useful for drug
 CC candidate screening. The present sequence is human IL-17 like protein.
 XX
 SQ Sequence 227 AA;

Query Match 99.1%; Score 1063; DB 22; Length 227;
 Best Local Similarity 100.0%; Pred. No. 6.9e-108; Indels 0; Gaps 0;
 Matches 195; Conservative 0; Mismatches 0;

Qy 3 LEPGLFLTLWHTCLAHDPSSLRGHPHSHGTPTHCYSAEELPLGQAPPHLLARGAKWGQAL 62
 Db 33 llpgllfltlwhtclahdpsslrghphshgtpchysaeelpgqapphllargakwgqal 92
 Qy 63 PVALVSSLEAAASHRGHERPSATTCQPVLRPEVLEADTHQRSISPWRYRVDTDDEYRPO 122
 Db 93 pvalvssleaaashrgtherpsattgcpvirpeevleadthqrsispwryrvdtdedrypq 152
 Qy 123 KLAFACELCRGCDARTGRETALNSVRLQSLVLLRRRPGSRDGSGLPTPGAFAPHTFE 182
 Db 153 klafaelcrgcdartgretalnsrvllqslvllrrrpscrdsqslptpgafafhtef 212
 Qy 183 IHVPVGCTCVLPVRSV 197
 Db 213 ihvpvgctcvlprsv 227

RESULT 13
 AAE08680
 ID AAE08680 standard; Protein; 227 AA.
 XX
 AC AAE08680;
 XX 15-NOV-2001 (first entry)
 DT Human interleukin (IL)-17 like protein mutant (Leu47Ile).
 DE
 XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
 KW multiple sclerosis; graft versus host disease; inflammatory disease;
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 47
 FT /note= "Wild-type Leu substituted with Ile"
 XX
 PN WO200159120-A2.
 XX 16-AUG-2001.
 XX
 PF 07-FEB-2001; 2001WO-US03916.
 PR 08-FEB-2000; 2000US-0180864.
 XX 27-NOV-2000; 2000US-0722920.
 PR (AMGE-) AMGEN INC.
 XX
 PI Jing S, Bass MB;
 XX WPI; 2001-529841/58.
 PT Novel interleukin-17 like polypeptides and nucleic acid molecules
 PT encoding them useful for diagnosis, prevention and treatment of
 PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
 PT rejection
 XX

PS Claim 18; Page -: 117pp; English.

XX The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Ile).

CC Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.

XX Sequence 227 AA;

 Query Match 98.9%; Score 1061; DB 22; Length 227;
 Best Local Similarity 99.5%; Pred. No. 1.1e-107;
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPLGLLFTWLHTCLAHDPDSLGRHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
 |||||
DB 33 Llpglflftwlhtclahdpdpslgrhpshtgtpchysaeelpgqapphllargakwgqal 92
 |||||

QY 63 PVALVSSLEAASHRGHERPSATTQCPVLPRPEVLADTHQRSISPWRYRVDDEDRYPQ 122
 |||||
DB 93 pvalvsleaashrgherpsattqcpvlrpeevleadthqrsispwryrvdtdedrypq 152
 |||||

QY 123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182
 |||||
DB 153 klafaeclrcgcidartgretaalnsrvllqslvlrrppcsrdsgslptpgafafhtef 212
 |||||

QY 183 IHVPVGCTCVLPKRSV 197
 |||||
DB 213 ihvpvgctcvlprsv 227
 |||||

RESULT 14
AAE08682
ID AAE08682 standard; Protein: 227 AA.
XX
AC AAE08682;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human interleukin (IL)-17 like protein mutant (Leu47Met).
XX
KW Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
KW multiple sclerosis; graft versus host disease; inflammatory disease;
KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.
XX
OS Homo sapiens.
OS
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Misc-difference 47 /note= "Wild-type Leu substituted with Met"
XX
PN WO200159120-A2.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US03916.
XX
PR 08-FEB-2000; 2000US-0180864.
XX
PR 27-NOV-2000; 2000US-072920.
PA (AMGE-) AMGEN INC.
XX
PI Jing S, Bass MB;
XX
DR WPI; 2001-529841/58.
XX
PT Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft rejection
XX
PS Claim 18; Page -: 117pp; English.
XX
CC The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Met).

CC Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.

XX Sequence 227 AA;

 Query Match 98.9%; Score 1061; DB 22; Length 227;
 Best Local Similarity 99.5%; Pred. No. 1.1e-107;
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPLGLLFTWLHTCLAHDPDSLGRHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
 |||||
DB 33 Llpglflftwlhtclahdpdpslgrhpshtgtpchysaeelpgqapphllargakwgqal 92
 |||||

QY 63 PVALVSSLEAASHRGHERPSATTQCPVLPRPEVLADTHQRSISPWRYRVDDEDRYPQ 122
 |||||
DB 93 pvalvsleaashrgherpsattqcpvlrpeevleadthqrsispwryrvdtdedrypq 152
 |||||

QY 123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182
 |||||
DB 153 klafaeclrcgcidartgretaalnsrvllqslvlrrppcsrdsgslptpgafafhtef 212
 |||||

QY 183 IHVPVGCTCVLPKRSV 197
Db 213 ihvpvgctcvlprsv 227

RESULT 15

AAE08681
ID AAE08681 standard; Protein: 227 AA.

XX AAE08681;

DT 15-NOV-2001 (first entry)

XX Human interleukin (IL)-17 like protein mutant (Leu47Val).

XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
KW multiple sclerosis; graft versus host disease; inflammatory disease;
KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 47 /note= "wild-type Leu substituted with Val"

FT WO200159120-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US03916.

XX 08-FEB-2000; 2000US-0180864.

XX 27-NOV-2000; 2000US-0722920.

XX (AMGE-) AMGEN INC.

XX Jing S, Bass MB;

XX WPI; 2001-529841/58.

XX Novel interleukin-17 like polypeptides and nucleic acid molecules
PT encoding them useful for diagnosis, prevention and treatment of
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
PT rejection

PS Claim 18; Page -: 117pp; English.

XX The present invention relates to interleukin (IL)-17 like polypeptides
and nucleic acids encoding them. IL-17 like protein is useful for
identifying binding partners, agonists and antagonists which can be used
for treating one or more diseases or disorders and for cloning IL-17
like receptors, using an expression cloning strategy. Radiolabelled or
affinity/activity-tagged IL-17 proteins are useful in binding assays to
identify a cell type or cell line or tissue that express IL-17 like
receptors. A radiolabelled or tagged IL-17 like protein is useful as an
affinity ligand to identify and isolate from an expression library the
subset of cells which express the IL-17 like receptors on their surface.
IL-17 like protein, agonist and antagonist are useful for treating acute
and chronic inflammation such as rheumatic diseases, graft versus host
disease and multiple sclerosis. IL-17 like antagonists are useful for
treating and preventing inflammatory disease, autoimmune disease,
allergies, asthma and organ or graft rejection in a patient and also
for inhibiting T cell proliferation and/or activation, in vivo B cell
proliferation or immunoglobulin secretion, and for blocking the effects
of IL-17 in inducing bone destruction. IL-17 like molecule is useful in
gene therapy and for mapping the location of the IL-17 like gene and
related genes on chromosomes, as hybridisation probes in diagnostic
assays. Non-human animals in which the promoter for one or more of IL-17
like protein is either activated or inactivated are useful for drug
candidate screening. The present sequence is human IL-17 like

CC protein mutant (Leu47Val).
CC Note: The present sequence is not shown in the specification, but is
CC derived from the human IL-17 like protein referred to as SEQ ID NO:2
CC (AAE08676), shown in figure 1A.
XX
SQ Sequence 227 AA;

Query Match 98.8%; Score 1060; DB 22; Length 227;
Best Local Similarity 99.5%; Pred. No. 1.5e-107;
Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPGLLFLTWLHTCLAHDPFSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
Db 33 LLPGLLFLTWLHTCVahdpSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 92
QY 63 PVALVSSLEAASHRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 122
Db 93 PVALVSSLEAASHRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 152
QY 123 KLAFACLCRCGICIDARTGRTAALNSVRLQLSLVLRPPCSRDGSGCLTPGAFAPFHTF 182
Db 153 klafaelcrgicidartgrettaalnsvrlqlslvrrppcsrdsgsltpgafafhtef 212
QY 183 IHVPVGCTCVLPKRSV 197
Db 213 ihvpvgctcvlprsv 227

Search completed: August 23, 2002, 16:01:48
Job time: 59 sec

DR	N ¹ -PSDB; RA4237426.
XX	
XX	
PT	New polypeptides designated PRO1031 and PRO1122 used to treat a
PT	degenerative cartilaginous disorder -
XX	
XX	Claim 23; Fig 3; 141pp; English.
PS	
XX	
XX	The present sequence is the human PRO1122 polypeptide, also referred to
CC	as UNO561, and as interleukin-17C (IL-17C), encoded by
CC	clone DNA623777-1381-1. This sequence has identity with the
CC	cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
CC	and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
CC	intestine, stomach and testis also. It shares about 26-28% amino acid
CC	identity with IL-17 and IL-17B. The entire coding region of IL-17C can
CC	be used as hybridisation probe. The PRO1122 polypeptide, agonist or
CC	antagonist, is used to diagnose and treat a degenerative cartilaginous
CC	disorder.
XX	
XX	Sequence 197 AA;
SQ	

Query Match	Best Local Similarity	Score 10/3;	DB 21;	Lengthn 197;
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTLLPGLLFTWLTCLAHHDPSLRGPHSHGTCHPCYSAAEELPLGQAPHLRLARGAKWGQ	60	
Db	1	mtllpgllftwtlhtclahhdpslrghpshgtchpcysaeelpglgqaphllargakwgq	60	
QY	61	ALPVALVSSLEAAASHRGRIHERFSATTQCPVLRPVEVLEADTHQRSISPWRYVDTDEDRY	120	
Db	61	alpvalvssleaaashrgriherfsattqcpvlrpeevleadthqrsispwryvdtdey	120	
QY	121	PQKLAFAECLRCGCDIARTGRTAALNSVRLQLQSLVLVLRPRCSRDGSGSLTTPGAFHFT	180	
Db	121	pklafaelrcqcdiartgretaalnsvrlqlslvlvrrpcsrddgsltpgafafht	180	

Qy	181	EFTHPVPGTCVLPRSV	197
		'	
Dd	181'	efihvpvgctcvlprsv	197

RESULT
6

AAAY53892	
ID	AAAY53892 standard; Protein; 197 AA.
XX	XX
AC	AAAY53892;
XX	XX
DT	13-MAR-2000 (first entry)
XX	XX
DE	Amino acid sequence of human interleukin-21.
XX	XX
KW	Human; Interleukin-22; IL-22; IL-21; immune system disorder;
KW	immune cell chemotaxis; haematopoietic cell disorder;
KW	haemostatic activity; thrombolytic activity; autoimmune disease; asthma;
KW	respiratory problem; organ rejection; graft-versus-host disease; GVHD;
KW	inflammation; hyperproliferative disorder; tissue regeneration;
KW	embryonic stem cell differentiation; embryonic stem cell proliferation;
KW	haematopoietic lineage; allergic asthma.

XX	Key	Location/Qualifiers
XX	Peptide	1..18
XX		/note= "signal peptide"
XX	Domain	34..40
XX		/note= "conserved domain V"
XX	Domain	63..68
XX		/note= "conserved domain VI"
XX	Domain	104..109
XX		/note= "conserved domain VII"
XX	Domain	113..121

~~Aug 25~~

FT FT /note= "conserved domain I"
 FT 129..134
 FT /note= "conserved domain II"
 FT 156..162
 FT /note= "conserved domain III"
 FT 185..192
 FT /note= "conserved domain IV"
 XX
 PN W09961617-A1.
 XX
 PD 02-DEC-1999.
 XX
 XX 27-MAY-1999; 99WO-US11644.
 XX
 PR 29-MAY-1998; 98US-0087340.
 PR 10-SEP-1998; 98US-009805.
 PR 30-APR-1999; 99US-0131965.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Ebner R;
 PI
 XX WPI: 2000-072622/06.
 DR N-PSDB; AA236836.
 DR
 XX Novel polynucleotides used to develop products for treating e.g. immune disorders, blood disorders, autoimmune disorders, allergies, inflammation, hyperproliferative disorders or infections
 PT
 PT
 PT
 XX
 PS Claim 26; Fig 6A-B; 170pp; English.
 XX
 CC The present sequence represents a human interleukin-21 (IL-21) protein. The specification also describes IL-22 polynucleotides and polypeptides. The IL-21 polynucleotide was isolated from a cDNA library of apoptotic T-cells. IL-21 and IL-22 may be useful in treating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies or disorders of haematopoietic cells, to modulate haemostatic or thrombolytic activity, in treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (GVHD), to modulate inflammation, to treat or detect hyperproliferative disorders, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the regeneration of tissues. IL-21 and IL-22 may also increase or decrease the differentiation or proliferation of embryonic stem cells and haematopoietic lineage, may be used to modulate mammalian characteristics.
 CC
 XX Sequence 197 AA;
 SQ

Query Match 100.08; Score 1073; DB 21; Length 197;
 Best Local Similarity 100.08; Pred. No. 4.6e-109;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTLPLGLFLTWLCLAHDPSPRGHSHGCTPHCYSAEELPLGQAPHLILARAKWGQ 60
 Dd 1 mtlplglflftwclclahdpsslrghshgtphcysaeelpgqapphlilargakwgq 60
 Qy 61 ALPVAVSSLEAASHRGHERPSATTQCPVLRPEVLEADTHORSISPRYRVDTDEDY 120
 Dd 61 alpvavssleashrgherpsattqcpvrpeevleadthqrsispryrvdtdedry 120
 Qy 121 POKLAFBCLRGCGIDARTGRTAALNSVRLIQSLVLRPPCSRDGSLPTPGAFAPHT 180
 Dd 121 pqklafaelcrgcldartgretaalnsrvllqslvlrrppcsrdsgslptpgafafht 180
 Qy 181 EFIHVPVCTCVLPRSV 197
 Dd 181 efihvpvgctcvlprsv 197

RESULT 7

AG66121
 ID AAG66121 standard; Protein; 197 AA.
 XX
 AC AAG66121;
 XX
 DT 13-MAR-2002 (first entry)
 XX
 DE Human interleukin (IL)-21 amino acid sequence.
 XX
 KW Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;
 KW antiinflammatory; antibacterial; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..18
 FT /note= "signal peptide"
 FT Protein
 FT 19..197
 FT /note= "mature protein"
 FT Domain
 FT 34..40
 FT /note= "conserved domain V"
 FT Domain
 FT 63..68
 FT /note= "conserved domain VI"
 FT Domain
 FT 104..109
 FT /note= "conserved domain VII"
 FT Domain
 FT 113..121
 FT /note= "conserved domain I"
 FT Domain
 FT 129..134
 FT /note= "conserved domain II"
 FT Domain
 FT 156..162
 FT /note= "conserved domain III"
 FT Domain
 FT 185..192
 FT /note= "conserved domain IV"
 XX
 US2001023070-A1.
 PD 20-SEP-2001.
 XX
 PF 08-DEC-2000; 2000US-0731816.
 XX
 PR 29-MAY-1998; 98US-087340P.
 PR 30-APR-1999; 98US-131965P.
 PR 09-DEC-1999; 99US-169837P.
 PR 27-MAY-1999; 99US-0320713.
 PR 27-MAY-1999; 99WO-US11644.
 XX
 PA (EBNE/) EBNER R.
 PA (RUBE/) RUBEN S M.
 XX
 PI Ebner R, Ruben SM;
 XX
 DR WPI: 2001-638470/73.
 DR N-PSDB; AA167878.
 XX
 PT New interleukin-21 and interleukin-22 polynucleotides and polypeptides,
 PT useful for treating, preventing or diagnosing e.g. disorders of
 PT hematopoietic cells, autoimmune disorders, or hyperproliferative
 PT diseases
 XX
 PS Claim 26; Fig 6A-B; 87pp; English.
 XX
 CC The invention relates to novel human proteins designated interleukin
 CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in
 CC linkage analysis as a marker for those specific chromosome, in chromosome
 CC mapping, to control gene expression through triple helix formation or
 CC antisense DNA or RNA, in gene therapy, in identifying individuals from
 CC minute biological samples, as an alternative to restriction fragment
 CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic
 CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and
 CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of
 CC the immune system by activating or inhibiting the proliferation,

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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:55 ; Search time 26.75 Seconds
(without alignments)
1274.019 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLPLGLFLTLWHTCLAHH.....FHTFTHVPVGCVCVLPFRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	Q9P0M4	Q9p0m4 homo sapien
2	1065	99.3	197	Q9HC75	Q9hc75 homo sapien
3	173	16.1	109	Q36P18	Q96p18 homo sapien
4	173	16.1	163	Q36PD4	Q96pd4 homo sapien
5	169.5	15.8	180	Q99MY3	Q99my3 mus musculus
6	168.5	15.7	180	Q9QXT6	Q9qxt6 mus musculus
7	165.5	15.4	177	Q9H293	Q9h293 homo sapien
8	160.5	15.0	215	Q9CTI4	Q9cti4 mus musculus
9	157.5	14.7	151	O40633	O40633 salmeline
10	157.5	14.7	178	Q9EQI6	Q9eqi6 mesocricetu
11	157	14.6	141	Q95L56	Q95l56 bos taurus
12	154.5	14.4	180	Q9UHF5	Q9uhf5 homo sapien
13	136	12.7	78	Q9NUE6	Q9nue6 homo sapien
14	129.5	12.1	111	Q9EQI7	Q9eqi7 rattus norv
15	110	10.3	148	Q19778	Q19778 caenorhabdi
16	95.5	8.9	93	Q9BEH5	Q9beh5 equus cabal

17	89.5	8.3	168	2	Q9XDC3	Q9xdc3 herbaspirill
18	89.5	8.3	521	12	Q9DP52	Q9dps2 meleagrid h
19	88.5	8.2	521	12	Q9E1H8	Q9elh8 meleagrid h
20	88	8.2	1548	4	Q9NYW9	Q9nyw9 homo sapien
21	88	8.2	2161	4	Q9Y566	Q9y566 homo sapien
22	86.5	8.1	389	10	Q9LEU1	Q9leul arabidopsis
23	86	8.0	297	2	Q99391	Q99391 streptomyce
24	86	8.0	1098	11	Q9JL71	Q9jl71 mus musculu
25	84.5	7.9	317	4	Q9BTV9	Q9btv9 homo sapien
26	84	7.8	179	10	Q93Z24	Q93z24 arabidopsis
27	84	7.8	354	10	Q9SE51	Q9se51 arabidopsis
28	82	7.6	313	3	Q9P795	Q9p795 schizosacch
29	82	7.6	415	10	Q9LGI3	Q9lgi3 oryza sativ
30	81.5	7.6	306	2	Q9L4D4	Q9l4d4 xanthomonas
31	81.5	7.6	380	5	Q9GSZ8	Q9gsz8 caenorhabdi
32	81	7.5	553	16	Q9I783	Q9i783 pseudomonas
33	80.5	7.5	283	5	Q9W4E1	Q9w4el drosophila
34	80.5	7.5	358	5	Q9U123	Q9u123 leishmania
35	80.5	7.5	638	4	Q9GLD4	Q9glld4 homo sapien
36	80	7.5	408	4	Q9GH86	Q9gh86 homo sapien
37	80	7.5	411	16	O86313	O86313 mycobacteri
38	79.5	7.4	681	5	Q95RM4	Q95rm4 drosophila
39	79.5	7.4	745	13	Q98SJ5	Q98sj5 brachydanio
40	79.5	7.4	1406	5	Q9V4D4	Q9v4d4 drosophila
41	79.5	7.4	1406	5	Q9U1I0	Q9u1i0 drosophila
42	79.5	7.4	1408	5	Q9XZU7	Q9xzu7 drosophila
43	79	7.4	465	4	Q9BWD7	Q9bwd7 homo sapien
44	79	7.4	837	4	Q9Y4R8	Q9y4r8 homo sapien
45	79	7.4	837	4	Q9BR21	Q9br21 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9P0M4	PRELIMINARY;	PRT;	197 AA.
AC	Q9P0M4;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	INTERLEUKIN 17C.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
QX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20105548; PubMed=10639155;			
RA	Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,			
RA	Gurney A.L., Wood W.I.;			
RT	"Cloning and Characterization of IL-17B and IL17C, Two New Members of			
RT	the IL-17 Cytokine Family";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).			
DR	EMBL; AF152099; AAF28105.1; -.			
SQ	SEQUENCE 197 AA; 21765 MW; BAB0152E18DE7D08 CRC64;			

Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.le-100;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTLLPGLFLTLWHTCLAHDPSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWQ	60
DB	1	MTLLPGLFLTLWHTCLAHDPSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWQ	60
QY	61	ALPVALVSLEAASHRGHERPSATTCQVLPREEVLEADTHQRSISPMWRYVVDDEDRY	120
DB	61	ALPVALVSLEAASHRGHERPSATTCQVLPREEVLEADTHQRSISPMWRYVVDDEDRY	120
QY	121	PKLFAECLRCGCDIARTGRTAALNSVRLQLLVLRRCRSDGGSLPTPGAFPH	180
DB	121	PKLFAECLRCGCDIARTGRTAALNSVRLQLLVLRRCRSDGGSLPTPGAFPH	180

Qy	177	AFHTEFIHVPVGCTV	192	
		:	:	
Db	164	QRVVMETIAVGCTCI	179	
RESULT	7			
Q9H293		PRELIMINARY;	PRT;	177 AA.
ID	Q9H293			
AC	Q9H293;			
DT	01-MAR-2001 (TEMBLrel. 16, Created)			
DT	01-MAR-2001 (TEMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	INTERLEUKIN 17E.			
GN	IL17E.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21125711; PubMed=11058597;			
RA	Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,			
RA	Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;			
RT	"IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolo-			
RT	g IL-17R β h.,"			
RL	J. Biol. Chem. 276:1660-1664(2001).			
DR	EMBL; AF305200; AAG40848.1;			
DR	SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;			
Query Match	15.4%;	Score	165.5;	DB 4; Length 177;
Best Local Similarity	29.7%;	Pred. No.	5.5e-09;	
Matches	52; Conservative	16; Mismatches	70; Indels	37; Gaps
Qy	27	HPHSHTGPHCYs-----AEEPLGQAPPHLLARGAKWGKQALVALVSSLEAASHRGRHER	81	
		:	:	
Db	31	HTYSHWPSCCPsRGQDTSEEL-----LRW-STVP---VPPEPARPNRHPES	73	
Qy	82	PSATTQCPVLRLPEVLEADTHORSISPRWYVDTDDEDRYPQKLAFAECILCRGCIADRTGR	141	
		:	:	
Db	74	CRASEDGLP-----NSRAISPRWYELDRDLRNLPODLYHARCILCHCVSLQTS	122	
Qy	142	ETAAL-NSVRLQLSLVRLRRPSCSDGSLPTPGAFATFTHVPVGCTCVLPR	195	
		:	:	
Db	123	HMDPRGNSELYHNQVYFRRPCHGEKG---THKGYCLERRLYRVSLACVCVRRP	174	
RESULT	8			
Q9CTI4		PRELIMINARY;	PRT;	215 AA.
ID	Q9CTI4			
AC	Q9CTI4;			
DT	01-JUN-2001 (TEMBLrel. 17, Created)			
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	I110006016RIK PROTEIN (FRAGMENT).			
GN	I117B OR I110006016RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK003506; BAB22826.1; -.
 DR MGD; MGI:1928997; I117b.
 FT NON_TER 1
 SQ SEQUENCE 215 AA; 24196 MW; 21468E7E01A92154 CRC64;

Query Match 15.0%; Score 160.5; DB 11; Length 215;
 Best Local Similarity 29.8%; Pred. No. 2.2e-08;
 Matches 48; Conservative 25; Mismatches 63; Indels 25; Gaps 5;

QY 45 GOAPPHLLARGAKWGQALPVALLVSSLEAASHRGHER-----PSATTQCPVL 91
 Db 66 GQRPSPLAGP---HOVPLDLVSRVKPYARMBEYERNLGEMVAQLRNISEPAKKKEV- 121
 QY 92 RPEVLEADTHQRSISPWRYRVDTDDEYRYPQKLAFAECICRGIDARTGRETAALNSVRL 151
 Db 122 ---NLQWLNSKRLSPWGYSLNHDPSPRIADLPPEARCLCLGCVNPFMTQEDRSWVSPV 178
 QY 152 LQSLVLRRCRSDGSLPTPGAFAFHTEFIHVPVGCCTV 192
 Db 179 F-SQVPRRLCPQP----PRPGCRQRVVMETIAGVCTCI 214

RESULT 9
 O40633 ID O40633 PRELIMINARY; PRT; 151 AA.
 AC O40633;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN 17.
 GN ORF13.
 OS Saimiriine herpesvirus 2.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=10381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-488;
 RX MEDLINE=98037620; PubMed=9371569;
 RA Knappe A., Hiller C., Thurnau M., Wittmann S., Hofmann H.,
 RA Fleckenstein B., Fickenscher H.,
 RT "The superantigen-homologous viral immediate-early gene iel4/vsag in
 RT herpesvirus saimiri-transformed human T cells.";
 RL J. Virol. 71:9124-9133(1997).
 DR EMBL; Y13183; CAAT3627.1; -.
 SQ SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 12; Length 151;
 Best Local Similarity 28.6%; Pred. No. 3e-08;
 Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALLVSSLEAASHRGHERPSATTQCPVLRPEE 95
 Db 18 CIVKSEITSATQPRCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
 QY 96 VLEADTHQRSISPWRYRVDTDDEYRYPQKLAFAECICRGIDARTGRETAALNSVRLQSL 155
 Db 61 ----DYNNRSTSPWTLRYNRDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMNSVPIQOEI 115

QY 156 LVLRR--RPSCRDGSGLPTPGAFAFHTEFIHVPVGCCTVLP 194
 Db 116 LVVRKGNPCPN-----SFRLEKMLVTVGCTCVTP 145

RESULT 10
 Q9EQI6 ID Q9EQI6 PRELIMINARY; PRT; 178 AA.
 AC Q9EQI6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
 RT "Identification of a novel IL-17 related factor: Demonstration of
 RT neuronal expression and evaluation as a candidate for the chromosome
 RT 5q-linked form of Charcot-Marie-Tooth disease.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF218725; AAG44134.1; -.
 FT NON_TER 178
 SQ SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;

Query Match 14.7%; Score 157.5; DB 11; Length 178;
 Best Local Similarity 29.5%; Pred. No. 3.6e-08;
 Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

QY 45 GOAPPHLLARGAKWGQALPVALLVSSLEAASHRGHERPSATTQCPVLRPEEVLAD---- 100
 Db 31 GOVRPGPLAGP---HQVPLDLVSRVKPYARMBEYERNLGEMVAQLRNSEPAKRRCEVN 87
 QY 101 ----THORSISPWRYRVDTDDEYRYPQKLAFAECICRGIDARTGRETAALNSVRLQSL 155
 Db 88 LQLWLSNKRSLSPWGYSLNHDPSPRIADLPPEARCLCLGCVNPFMTQEDRSWVSPV-SQ 146
 QY 156 LVLRRRPSCRDGSGLPTPGAFAFHTEFIHVPVGCCTC 191
 Db 147 VPVRRRLCPQP----PRPGCRHRVVMETIAGVCTC 178

RESULT 11
 Q95L56 ID Q95L56 PRELIMINARY; PRT; 141 AA.
 AC Q95L56;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN 17 (FRAGMENT).
 GN IL17.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee I.-K., Mwangi S.M., Olsen S., Kehrli M. Jr.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF416586; AAL08013.1; -.
 FT NON_TER 1
 FT CHAIN 11 141 INTERLEUKIN 17.
 SQ SEQUENCE 141 AA; 15945 MW; 94077A79DD803F3E CRC64;

Query Match 14.6%; Score 157; DB 6; Length 141;

[illegible]

RT "Identification of a novel IL-17 related factor: Demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF218724; AAG44133.1; -

FT NON_TER 1 1

FT NON_TER 111 111

SQ SEQUENCE 111 AA; 12628 MW; D1598992981BA867 CRC64;

Query Match 12.1%; Score 129.5; DB 11; Length 111;
Best Local Similarity 37.8%; Pred. No. 1.4e-05;
Matches 28; Conservative 16; Mismatches 25; Indels 5; Gaps 2;

QY 101 THORISPMRYRVDTDEDYPOKLAFAECLRCGCDARTGRTAALNSVRLQLSLVLR 160

Db ::::||||| : : : | : | | | | : : | : : | : : | : : | : : | : : |

30 SNKRSLSPMGYSTINHPDRIPEDLPARCLCLGCVNPFTMQEDRSMSVVPVF-SQVPVRR 88

QY 161 RPCSRDGSGLPTPG 174

Db | : : | : |

89 RLCPOP-PRPG 98

RESULT 15

Q19778

ID Q19778 PRELIMINARY; PRT; 148 AA.

AC Q19778;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE F25D1.3 PROTEIN.

GN F25D1.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Kelly P.F.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";

RL Science 282:2012-2018(1998).

DR EMBL: Z73973; CAA98268.1; -

SQ SEQUENCE 148 AA; 16738 MW; ADB51F438DFB3940 CRC64;

Query Match 10.3%; Score 110; DB 5; Length 148;
Best Local Similarity 33.0%; Pred. No. 0.0018;
Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;

QY 103 QRSISPMRYRVDTDEDYPOKLAFAECLRCGCDARTGRTAALNSVRLQLSLVLR 162

Db ::::||||| : : : | : | | | | : : | : : | : : | : : | : : |

51 ERALCPWDSRVNQESREPKIAESVCLC-----RKSRGSTGAFCMPIVRKVPILRRVS 104

QY 163 CSRDGSGLPTPGAFAPHTFEIHVPVCCVLP 196

Db | : : | : | : | | | | | | | | | |

105 CDR-STGL---WNVVRSTELI--TVGCHSVLPRT 132

Search completed: August 23, 2002, 16:03:07
Job time: 132 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:55 ; Search time 11.96 Seconds
(without alignments)
637.772 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLPLGLLFLTWLHTCLAHH.....FHTEFIHVPVGCRCVLPVRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	1073	100.0	197	1	I17C_HUMAN	Q9p0m4 homo sapien
2	173	16.1	153	1	I17F_HUMAN	Q96pd4 homo sapien
3	168.5	15.7	180	1	I17E_MOUSE	Q9qxt6 mus musculus
4	165.5	15.4	177	1	I17E_HUMAN	Q9h293 homo sapien
5	160.5	15.0	151	1	V613_HSVSA	P24916 herpesvirus
6	158	14.7	155	1	I17_HUMAN	Q16552 homo sapien
7	157.5	14.7	151	1	V613_HSVSC	O40633 herpesvirus
8	137.5	14.7	178	1	I17B_MESAU	Q9eq16 mesocricetu
9	134.5	14.4	180	1	I17B_HUMAN	Q9uhf5 homo sapien
10	148.5	13.8	150	1	I17_RAT	Q61453 rattus norv
11	148.5	13.8	158	1	I17_MOUSE	Q62386 mus musculus
12	85.5	8.0	465	1	HNF6_HUMAN	O9ubc0 homo sapien
13	85.5	8.0	465	1	HNF6_MOUSE	O08755 mus musculus
14	85.5	8.0	465	1	HNF6_RAT	P70512 rattus norv
15	84.5	7.9	1638	1	BRM_DROME	P25439 drosophila
16	82.5	7.7	635	1	GIDA_SYNY3	Q55694 synchocyst
17	81.5	7.6	325	1	HM06_CAEEL	P20268 caenorhabdi
18	79	7.4	549	1	FAST_HUMAN	Q14296 homo sapien
19	77.5	7.2	323	1	FR2A_CHICK	P18625 gallus gall
20	77.5	7.2	581	1	TR14_HUMAN	Q15650 homo sapien
21	76.5	7.1	503	1	PR19_YEAST	P32523 saccharomyc
22	74.5	6.9	639	1	DNK7_HUMAN	Q09013 homo sapien
23	74	6.9	260	1	TNR7_HUMAN	P26842 homo sapien
24	74	6.9	976	1	EPAL_HUMAN	P21709 homo sapien
25	74	6.9	2842	1	APC_RAT	P70478 rattus norv
26	73.5	6.8	559	1	HNF6_PIG	Q03365 mus scrofa
27	73.5	6.8	741	1	NFL1_MOUSE	Q61985 mus musculus
28	73	6.8	373	1	DDL_MYCTU	P95114 mycobacteri
29	72.5	6.8	466	1	DDL_CHICK	P23824 gallus gall
30	72.5	6.8	528	1	CP15_CHICK	P79761 gallus gall
31	72.5	6.8	772	1	NFL1_HUMAN	Q14494 h nuclear f
32	71.5	6.7	203	1	COBC_ECOLI	P52086 escherichia
33	71.5	6.7	214	1	VEGA_CANFA	Q9myv3 canis famil

34 71.5 6.7 297 1 HXAB_CHICK
35 71.5 6.7 433 1 PMEB_ERWCH
36 71 6.6 322 1 FOS_AVINK
37 71 6.6 342 1 CRTB_STRGR
38 71 6.6 367 1 FOS_CHICK
39 71 6.6 2564 1 SPCQ_HUMAN
40 70.5 6.6 256 1 KPTA_AERPE
41 70.5 6.6 313 1 HXAB_MOUSE
42 70.5 6.6 705 1 PIXB_MOUSE
43 70 6.5 381 1 SLP_HUMAN
44 70 6.5 411 1 HOX3_BRAFL
45 70 6.5 839 1 ZF95_HUMAN

ALIGNMENTS

RESULT 1
I17C_HUMAN
ID I17C_HUMAN STANDARD; PRT; 197 AA.
AC Q9P0M4; Q9HC75;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).
GN IL17C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20105548; PubMed=10639155;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., He L., Wan T., Yuan Z., Cao X.;
RT "Novel human cytokine CX2 with homology to IL-17";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF152099; AAF28105.1;
CC EMBL; AF142410; AAG27921.1;
CC MIM; 604628; -;
DR EMBL; AF152099; AAF28105.1;
DR EMBL; AF142410; AAG27921.1;
DR MIM; 604628; -;
KW Cytokine; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 197 INTERLEUKIN-17C.
FT DISULFID 129 189 BY SIMILARITY.
FT DISULFID 134 191 BY SIMILARITY.
FT CONFLICT 50 50 H -> R (IN REF. 2).
SQ SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;

Query Match 100.0%; Score 1073; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.4e-94;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTLPLGLLFLTWLHTCLAHDPVSLRGPHSHCTPHCYSAEELPLGQAPPHLLARGAKMQ 60

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Db 1 MTLLPGLLEFTWLTCLAHDPSELGRPHSHGTPHCYSABEPLDGLQAPPHLARGAKWGQ 60
QY 61 ALPVALVSSLEAAASHGRHERPSATTQCPVLRPEEVELEADTHORSISPMRYRVDTDEDY 120
Db 61 ALPVALVSSLEAAASHGRHERPSATTQCPVLRPEEVELEADTHORSISPMRYRVDTDEDY 120
QY 121 POKLAFACLCRCIDARTGRTAALNSVRLQSLVLRRLRRPCSRDGSGLPTPGAFAFHT 180
Db 121 POKLAFACLCRCIDARTGRTAALNSVRLQSLVLRRLRRPCSRDGSGLPTPGAFAFHT 180
QY 181 EFTHPVVGCTCVLPVRSV 197
Db 181 EFTHPVVGCTCVLPVRSV 197

RESULT 2
IL17F_HUMAN STANDARD; PRT; 153 AA.
AC Q96PD4; Q9NUE6; Q96PI8;
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Interleukin-17F precursor (IL-17F) (Interleukin-24) (Cytokine ML-1).
GN IL17F OR IL24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21475830; PubMed=11591732;
RA Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
RA Broxmeyer H.E., Hromas R.;
RT "IL-17F, a novel cytokine selectively expressed in activated T cells
RT and monocytes, regulates angiogenesis and endothelial cell cytokine
RT production.";
RL J. Immunol. 167:4137-4140(2001).
RN [2]
RP SEQUENCE OF 2-153 FROM N.A.
RX MEDLINE=21475866; PubMed=11591768;
RA Kawaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
RA Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
RT "Identification of a novel cytokine, ML-1, and its expression in
RT subjects with asthma.";
RL J. Immunol. 167:4430-4435(2001).
RN [3]
RP SEQUENCE OF 76-153 FROM N.A.
RA Almeida J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION.
RX PubMed=11574464;
RA Hymowitz S.G., Filvaroff E.H., Yin J.P., Lee J., Cai L., Risser P.,
RA Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L.,
RA De Vos A.M., Starovasinik M.A.;
RT "IL-17s adopt a cysteine knot fold: structure and activity of a novel
RT cytokine, IL-17F, and implications for receptor binding.";
RL EMBO J. 20:5332-5341(2001).
CC -!- FUNCTION: Stimulates the production of other cytokines such as IL-
CC 6, IL-8 and granulocyte colony-stimulating factor, and can
CC regulate cartilage matrix turnover. Stimulates PBMC and T-cell
CC proliferation. Inhibits angiogenesis.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in activated, but not resting, CD4+
CC T cells and activated monocytes.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC
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CC or send an email to a license@isb-sib.ch).
CC
CC EMBL: AF384857; AAK83350.1; ALT INIT.
CC EMBL: AF332389; AAL14427.1; ALT_INIT.
CC EMBL: AL034343; CAB75300.1; -.
DR PDB; 1JPY; 28-SEP-01.
DR MIM; 606496; -.
KW Cytokine; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 20 POTENTIAL
FT CHAIN 21 153 INTERLEUKIN-17F.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...);
FT DISULFID 37 37 INTERCHAIN (WITH C-127').
FT DISULFID 92 142
FT DISULFID 97 144
FT DISULFID 127 127 INTERCHAIN (WITH C-37').
SQ SEQUENCE 153 AA; 17009 MW; BB489BED863D57CE CRC64;

Query Match 16.1%; Score 173; DB 1; Length 153;
Best Local Similarity 39.0%; Pred. No. 1.7e-09;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPMRYRVDTDEDYPOKLAFAECLRCGCDARTGRTAALNSVRLQSL 156
Db 60 MSRNIESRSTSPWNYTWTWDPNRPSEVQAQCRNLGCIINAQ-GKEDISMNSVPIQOETL 118
QY 157 VLRRR-PCSRDGSGLPTPGAFAFHTFTHVPVGCCTVLP 194
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVTP 147

RESULT 3
IL17B_MOUSE STANDARD; PRT; 180 AA.
AC Q9QXT6; Q99MY3; Q9CTI4;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYTO7)
DE (Neuronal interleukin-17 related factor) (Cytokine CX1).
GN IL17B OR ZCYTO7 OR N1RF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Zhang W., Cao X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RESULT

ID	IL-17E_HUMAN	STANDARD;	PRT;	177 AA.
Q9H293;				
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-17E precursor (IL-17E).			
GN	IL17E.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RZ	SEQUENCE FROM N.A.			
XX	MEDLINE_21125711; PubMed=11058597;			
RA	Lee J., Ho W.-H.; Marucka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.; "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17Rhl."; J. Biol. Chem. 276:1660-1664(2001). -			
CL	-I- FUNCTION: Induces activation of NF-kappaB and stimulates production of the proinflammatory chemokine IL-8. -			
CC	-I- SUBCELLULAR LOCATION: Secreted. -			
CC	-I- TISSUE SPECIFICITY: Expressed at low levels in several tissues, including brain, kidney, lung, prostate, testis, spinal cord, adrenal gland, and trachea. -			
CC	-I- SIMILARITY: BELONGS TO THE IL-17 FAMILY. -----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensel@sb-sib.ch). -----			
DR	EMBL; AF305200; AAC40848.1; -			
DR	MMW; 605658; --			
KW	Cytokine; Glycoprotein; Signal.			
FT	SIGNAL 1 32 POTENTIAL.			
FT	CHAIN 33 177 INTERLEUKIN-17E.			
FT	DISULFID 110 168 BY SIMILARITY.			
FT	DISULFID 115 170 BY SIMILARITY.			
FT	CARBOHYD 136 136 N-LINKED (GLCNAC...) (POTENTIAL). SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;			
SQ				
Query Match 15.4%; Score 165.5; DB 1; Length 177;				
Best Local Similarity 29.7%; Pred.No. 1e-08;				
Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;				
QY	27 HPISHGTTPHCYS-----AEELPLQGAPPHLLARGAKWGQALPVAVSSLEAASHRGHER 81	:	: :	: :
Db	31 HTSYHWSPSCPSKGODTSSEL-----LRW-STVP---VPPLEPARPNRHPE 73	:	: :	: :
QY	82 PSATTQCPLVRPERVEADTHQRISPWRVTDDRYDPKLAFABLCRCGCIDATGR 141	:	: :	: : :
Db	74 CRASEDGPL-----NSRAISPWRVELRDRLNPQLDYHARCCLPGCVSLQTGS 122	:	: :	: : :
QY	142 ETAAL-NSVRLLOSLVLRRRPCSRDSGLPTTGCAFAFTEHTFPVGCTCFLPR 195	:	: :	: : :
Db	123 HM DPRGNSELYNQTVFYRPCHGEKG----THGYCLERRLYRVSLACVCVRPR 174	:	: :	: : :

RESULT

ID	VGI3_HSVA	STANDARD;	PRT;	151 AA.
DC	VGI3_HSVA			
AC	P24916;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			

RESULT	6
ID IL17_HUMAN	
ID IL17_HUMAN	STANDARD; PRT; 155 AA.
AC Q16552;	
DT 01-NOV-1997	(Rel. 35, Created)
DT 01-NOV-1997	(Rel. 35, Last sequence update)
DE 01-MAR-2002	(Rel. 41, Last annotation update)
DE Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).	
GN IL17 OR IL17A OR CTLA8.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=96281911; PubMed=8676080;	
RA Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Ait-Yahia S., Meat C., Pin J.-J., Garrone P., Garcia E., Saeland S., Blanchard D., Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J., Lebecque S.;	
RA "T cell interleukin-17 induces stromal cells to produce proinflammatory and hematopoietic cytokines.";	
J. Exp. Med. 183:2593-2603(1996).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC TISSUE=T-cell;	
RX MEDLINE=96094436; PubMed=7499828;	
RA Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M., Spriggs M.K., Armitage R.J.;	
RA "Human IL-17: a novel cytokine derived from T cells.";	
J. Immunol. 155:5483-5486(1995).	
CC -!- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.	
CC -!- SUBUNIT: HOMODIMER.	
CC -!- SUBCELLULAR LOCATION: Secreted.	
CC -!- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.	
CC -!- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.	
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.	
CC -!- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL17; WWW:"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=211".	

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DR EMBL; Z58820; CAAG1233.1; --	
DR EMBL; U32659; AAC50341.1; --	
DR MIM; 603149; --	
KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.	
FT SIGNAL 1 23 POTENTIAL.	
FT CHAIN 24 155 INTERLEUKIN-17.	
FT DISULFID 94 144 BY SIMILARITY.	
FT DISULFID 99 146 BY SIMILARITY.	
FT CARBOHYD 68 68 N-LINKED (GLCNAC...) (POTENTIAL).	
SQ SEQUENCE 155 AA; 17504 MW; 2BCAE9CB2F4886D1 CRC64;	
Query Match 14.7%; Score 158; DB 1; Length 155;	
Best Local Similarity 39.8%; Pred. No. 4.5e-08;	
Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;	
QY 99 ADTHORSISPWRYRVDTEDEYRYPKLAFAECLRCGCDARTGRETAALNSVRLQLSLVL 158 : : : : : : : : : : :	
Dd 64 SDYNRTSTPNWLHRNDDPERYSVIWEAKRHLCGCINA-DGNVDYMINSVP IQEILVL 122 : : : : : :	
QY 159 RRPR--CSRDSGSLPTPGAFHFTEFHVPVGTCTVLP 194 : : : : : :	

RESULT	8
IL17B_MESAU	
ID	IL17B_MESAU
STANDARD;	
PRT;	178 AA.
AC	Q9EQ16;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Interleukin-17B precursor (IL-17B) (Neuronal interleukin-17 related factor) (Fragment).

[illegible]

FT CONFLICT 46 46 I -> L (IN REF. 3).
SQ SEQUENCE 150 AA; 16876 MW; EF13F33EDF9D689F CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 150;
Best Local Similarity 29.4%; Pred. No. 3.4e-07;
Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;
Qy 42 LPLGQAPHLARGAKWGQALPVSLVSSLEASHGRHSPSATTCQPLRPEEVLADT 101
Db 21 IPOSSVCNAENNFONVKNLKVNSL---SSRASSRRPS-----DY 61
Qy 102 HORSISPRYRVDTDEDYPOKLAFAECLRCGCDARTGRETAAALNSVRLQLSLVLR 161
Db 62 LNRSTSPWTLNRNEDPDYPSVIAEQACRQRCVNAE-GKLDHMHNSVLIOEILVLKRE 120
Qy 162 P-CSRDGSLPTGCAFAFTEFIHVPVGCCTV 192
Db 121 PEKC-----PFTFRVKMLVGVGCTCV 142

RESULT 11
IL17_MOUSE
ID IL17_MOUSE STANDARD; PRT; 158 AA.
AC Q62386; Q60971;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).
DE IL17 OR CTLA8.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Thymocytes;
RX MEDLINE=97031826; PubMed=887732;
RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,
RA Wagner J.L., Hannum C.H., Zlotnik A.;
RT "Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR +
CD4-CD8- T cells.";
RL J. Interferon Cytokine Res. 16:611-617(1996).
RN [2]
RP SEQUENCE OF 12-158 FROM N.A.
RC STRAIN=129/SV; TISSUE=T-cell;
RX MEDLINE=96194901; PubMed=8654948;
RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;
RT "Complete nucleotide sequence of the mouse CTLA8 gene.";
RL Gene 168:223-225(1996).
CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
HEMATOPOIETIC CYTOKINES (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

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EMBL; U43088; AAB05222.1; -;
DR EMBL; U35108; AAA93253.1; -;
DR MGI; 107364; IL17.
KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 158
FT DISULFID 97 147
BY SIMILARITY.

FT DISULFID 102 149 BY SIMILARITY.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 158 AA; 17490 MW; 3505C14345F4653 CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 158;
Best Local Similarity 37.6%; Pred. No. 3.6e-07;
Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;
Qy 92 RPEEVLADTHORSISPRYRVDTDEDYPOKLAFAECLRCGCDARTGRETAAALNSVRL 151
Db 65 RPSDYL-----NRSTSPWTLNRNEDPDYPSVIAEQACRQRCVNAE-GKLDHMHNSVLI 118
Qy 152 LOSLVLVLRRRPGRDGLPTGCAFAFTEFIHVPVGCCTV 192
Db 119 QOEILVLKREPES-----CPFTFRVKMLVGVGCTCV 150

RESULT 12
HNF6_HUMAN
ID HNF6_HUMAN STANDARD; PRT; 465 AA.
AC Q9UBC0; Q9UMR6; Q97744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).
GN ONECUT1 OR HNF6A OR HNF6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Furuta H., Horikawa Y., Wang Y.-O., Bell G.I.;
RT "Isolation and characterization of the human hepatocyte nuclear factor
6 gene.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Furuta H., Wang Y.-O., Bell G.I.;
RT "The sequence of human mRNA for the hepatocyte nuclear factor-6
alpha.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-368 FROM N.A., AND VARIANT ALA-75.
RX MEDLINE=99420592; PubMed=10491763;
RA Moeller A.M., Ek J., Durvieux S.M., Urhammer S.A., Clausen J.O.,
RA Eiberg H., Hansen T., Rousseau G.G., Lemaire F.P., Pedersen O.;
RT "Hepatocyte nuclear factor-6: associations between genetic variability
and type II diabetes and between genetic variability and estimates of
insulin secretion.";
RL Diabetologia 42:1011-1016(1999).
RN [4]
RP SEQUENCE OF 174-465 FROM N.A.
RA Samadani U., Costa R.H.;
RT "Yeast one-hybrid cloning of the partial human cDNA for hepatocyte
nuclear factor 6.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE
5'-DHATGATGATWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE
OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION.
CC -1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER; LOWER EXPRESSION IN
TESTIS AND SKIN.
CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.

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or send an email to license@isb-sib.ch).

EMBL; U43088; AAB05222.1; -;
DR EMBL; U35108; AAA93253.1; -;
DR MGI; 107364; IL17.
KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 158
FT DISULFID 97 147
BY SIMILARITY.

CC entities requires a license agreement. (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

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DR EMBL: AF035581; AAD02033.1; -.
DR EMBL: AF035580; AAD02033.1; JOINED.
DR EMBL: U96173; AAD00826.1; -.
DR EMBL: Y17739; CAB50769.1; -.
DR EMBL: U77975; AAB61705.1; -.
DR TRANSFAC; T03286; -.
DR MIM; 604164; -.
DR InterPro: IPR003350; CUT.
DR InterPro: IPR001356; Homeobox.
DR Pfam; PF02376; CUT; 1.
DR Pfam; PF00046; homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
KW Activator; Polymorphism.
FT DNA_BIND 283 369
FT DNA_BIND 385 444
FT DOMAIN 69 72
FT DOMAIN 124 138
FT DOMAIN 455 460
FT VARIANT 75 75
FT CONFLICT 220 220 A -> T (IN REF. 3 AND 4).
FT CONFLICT 284 284 S -> N (IN REF. 4).
FT CONFLICT 288 288 Q -> H (IN REF. 4).
FT CONFLICT 318 318 R -> K (IN REF. 4).
FT CONFLICT 386 386 K -> Q (IN REF. 4).
SQ SEQUENCE 465 AA; 51023 MW; F47F78957A6ECFC2 CRC64;

Query Match 8.0%; Score 85.5; DB 1; Length 465;
Best Local Similarity 25.8%; Pred. No. 1;
Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHDPSSLRGPHSHGPHCYSAEELPLGQAPP-----HLLARGAKWGQALPVALVSSLEA 72
Db 220 AHPMLGRHGEQHLTP--TSAGMVPINGLPHPHHAHLNAQG--HGQLLGTA-----268

QY 73 ASHRGRHERPSAT-----TQCPVLRPEVLEADTHORSISPRYRVDTDEDY-- 120
Db 269 -----REPNPSTVGAOVNSGNSGQMEINTKEVAQ-----RITTELKRYSI 310

QY 121 POKLAFACLCR--GCID-----ARTGRETAALNSVRL-----LQSLVLVR 159
Db 311 PQAIFAQVLCRSQGTSLDLLRNPKPWSKLKSGRETFR----RMWKWLOEPEFORMSALR 366

QY 160 RRPCSR 165
Db 367 LAACKR 372

RESULT 13
HNF6_MOUSE
ID HNF6_MOUSE STANDARD; PRT; 465 AA.
AC O08755;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).
GN ONECUT1 OR HNF6A OR HNF6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Samadani U., Rausa F., Costa R.H.;
RT "Mouse hepatocyte nuclear factor-6 cDNA.";
```


RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=96382488; PubMed=8790352;
 RA Lemaigre F.P., Durvieux S.M., Truong O., Lannoy V.J., Hsuan J.J.,
 RA Rousseau G.G.;
 RT "Hepatocyte nuclear factor 6, a transcription factor that contains a
 RT novel type of homeodomain and a single cut domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:9460-9464(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=Wistar;
 RX MEDLINE=98256275; PubMed=9593691;
 RA Lannoy V.J., Buerklin T.R., Rousseau G.G., Lemaigre F.P.;
 RT "Isoforms of hepatocyte nuclear factor-6 differ in DNA-binding
 RT properties, contain a bifunctional homeodomain, and define the new
 RT ONECUT class of homeodomain proteins.";
 RL J. Biol. Chem. 273:13552-13562(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=97042457; PubMed=8887657;
 RA Samadani U., Costa R.H.;
 RT "The transcriptional activator hepatocyte nuclear factor 6 regulates
 RT liver gene expression.";
 RL Mol. Cell. Biol. 16:6273-6284(1996).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE
 CC 5'-DHATTGATTTWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE
 CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION. THE
 CC AFFINITY OF HNF-6ALPHA AND HNF-6BETA FOR DNA DIFFERS DEPENDING ON
 CC THE TARGET SEQUENCE.
 CC -1- SUBUNIT: BINDS DNA AS A MONOMER.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN, SPLEEN AND TESTIS.
 CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X96553; CAA65389.1; -
 CC EMBL: Y14933; CAA75150.1; -
 CC TRANSFAC: T03257; -
 CC InterPro: IPR003350; CUT.
 CC InterPro: IPR001356; Homeobox.
 CC Pfam: PF02376; CUT; 1.
 CC Pfam: PF00046; homeobox; 1.
 CC SMART: SM00389; HOX; 1.
 CC PROSITE: PS00027; HOMEBOX_1; FALSE_NEG.
 CC PROSITE: PS50071; HOMEBOX_2; 1.
 CC Transcription regulation: Homeobox; DNA-binding; Nuclear protein;
 KW Activator; Alternative splicing.
 FT DNA_BIND 283 369 CUT
 FT DNA_BIND 385 444 HOMEBOX.
 FT DOMAIN 69 72 POLY-HIS.
 FT DOMAIN 124 138 POLY-HIS.
 FT DOMAIN 455 460 POLY-SER.
 FT VARSPLIC 368 368 A -> AESAMGSSVPSLRITSSGGPQLSVPPPLP (IN
 FT ISOFORM BETA)
 SQ SEQUENCE 465 AA; 51067 MW; BD651267ED7AC896 CRC64;

Query Match 8.0%; Score 85.5; DB 1; Length 465;
 Best Local Similarity 25.8%; Pred. No. 1;
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

Db 220 AHPAMLRGHEQHLTP--TSAGMVPINGLPPHPHHLNAQGG--HGQLLGT----- 268
 QY 73 ASHRGHERPSAT-----TQCPVLPEEVLEADTHQRSISPWRYRVDTDREY-- 120
 Db 269 -----REPNSPTGAQVNSGNGMEEINTKEVAQ-----RIITLEKRYYSI 310
 QY 121 POKLAFACLCR--GCID-----ARTGRETAALNSVRL-----LQSLVLVR 159
 Db 311 PQAIFAQVLCRSQGLDLSLLRNPKWPKLKSRETFR-----RMWKWLQEPFQMSALR 366
 QY 160 RRPCSR 165
 Db 367 LAACKR 372
 RESULT 15
 BRML_DROME
 ID BRML_DROME STANDARD: PRT; 1638 AA.
 AC P25439; Q9VUW5; Q9VUW6;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Homeotic gene regulator (Brahma protein).
 GN BRM OR CG5942 OR CG18438.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RX MEDLINE=92154670; PubMed=1346755;
 RA Tankun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M.,
 RA Kaufman T.C., Kennison J.A.;
 RT "Brahma: a regulator of Drosophila homeotic genes structurally
 RT related to the yeast transcriptional activator SNF2/SWI2.";
 RL Cell 68:561-572(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe W., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:54 ; Search time 19.69 Seconds
(without alignments)
961.381 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: ~ 1073
Sequence: 1 MTLLPGLLFTWLHTCLAHH.....FHTFTHVPGVCTCVLP RSV 197

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160.5	15.0	151	B45351	immediate-early pr
2	148.5	13.8	147	JC4628	cytotoxic T-lympho
3	148.5	13.8	150	I49623	cytotoxic T-lympho
4	110	10.3	148	T21334	hypothetical prote
5	93.5	8.7	395	K1SMG	galactokinase (EC
6	86.5	8.1	389	T50809	hypothetical prote
7	86	8.0	297	JL0032	hypothetical 31.7K
8	84.5	7.9	1638	A42091	transcription acti
9	82.5	7.7	635	T76371	hypothetical prote
10	81.5	7.6	325	T23218	hypothetical prote
11	81	7.5	553	D83640	hypothetical prote
12	80.5	7.5	210	B40203	4-alpha-glucanotra
13	80	7.5	411	A70509	hypothetical prote
14	79.5	7.4	638	JC7753	ring finger B-box
15	79	7.4	549	I37386	fas-activated seri
16	79	7.4	837	T12514	hypothetical prote
17	79	7.4	885	T75894	hypothetical prote
18	78.5	7.3	132	E27603	hypothetical prote
19	78	7.3	309	T37033	hypothetical prote
20	77.5	7.2	209	T30698	hypothetical prote
21	77.5	7.2	323	A35909	fra-2 protein - ch
22	77.5	7.2	567	E96784	ethylene-insensiti
23	77	7.2	420	T14166	fxuD protein - Myc
24	77	7.2	466	T36212	replication initia
25	77	7.2	639	T97670	beta-n-acetylhexos
26	77	7.2	639	AC2895	beta-N-acetylhexos
27	76.5	7.1	405	G84338	3-hydroxy-3-methyl
28	76.5	7.1	503	S64787	pre-mRNA splicing
29	76.5	7.1	1882	T00069	hypothetical prote

ALIGNMENTS

RESULT 1

B45351
Immediate-early protein 2 - saimirine herpesvirus 1 (strain 11)
N:Alternate names: hypothetical protein ORF13
C:Species: saimirine herpesvirus 1
A:Note: host Saimiri sciureus (common squirrel monkey)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: B45351; D36807
R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.
Virolgy 179, 189-200, 1990
A:Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties
A:Reference number: A45351; MUID:91021021
A:Accession: B45351
A:Molecule type: mRNA
A:Residues: 1-151 <NIC>
A:Cross-references: GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:g331042
R:Albrecht, J.
submitted to the EMBL Data Library, January 1992
A:Description: Primary structure of the herpesvirus saimiri genome.
A:Reference number: A36806
A:Accession: D36807
A:Molecule type: DNA
A:Residues: 1-151 <ALB>
A:Cross-references: GB:X64346; NID:g60320; PIDN:CAA45636.1; PID:g60334
R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;
J. Virol. 66, 5047-5058, 1992
A:Title: Primary structure of the herpesvirus saimiri genome.
A:Reference number: A37309; MUID:92333688
A:Contents: annotation; protein-coding frames
A:Note: neither protein nor nucleotide sequence is given
C:Genetics:
A:Gene: 13
C:Superfamily: saimiri herpesvirus immediate-early protein 2
C:Keywords: early protein

Query Match 15.0%; Score 160.5; DB 1; Length 151;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY	36	CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAAASHRGHERPSATTQCVLRPEE	95
DB	18	CIIVKSEIYSAQTPRCALAA-----NNSFPRSVMTLSIRNWTSSKRAS-----	60
QY	96	VLEADTHORSIPWRYVDTDDEYRYPQKLAFAECILCRGICDARTGRTAALNSVRLQSL	155
DB	61	----DYNNRSTSPWTLHRNQDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMNSVPIQOEI	115
QY	156	LVLRR--RPSRDGSGGLTTPGAFATHTFIHVPVCTCVLP	194
DB	116	LIVRKGHGPCN-----SPFLEKMLVTVGCTCTVP	145

probable oxidoredu
hypothetical prote
sensory box sensor
hypothetical prote
protein kinase (EC
hypothetical prote
CD27 antigen precu
hypothetical 37.5K
transcription fact
probable transcrip
hypothetical prote
probable ddla - My
lacta protein - Li
hypothetical prote
hypothetical prote
transcription fact

Db 303 A---ARRLPHLLP-RAGPGRRHGPGLRGP 327

RESULT 6

T50809 hypothetical protein T30N20_270 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T50809

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25240

A:Accession: T50809

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <BEV>

A:Cross-references: EMBL:AL365234

A:Experimental source: cultivar Columbia; BAC clone T30N20

C:Genetics:

A:Map position: 5

A:Note: T30N20_270

Query Match 8.1%; Score 86.5; DB 2; Length 389;

Best Local Similarity 23.0%; Pred. No. 2.3;

Matches 56; Conservative 25; Mismatches 83; Indels 79; Gaps 10;

QY 6 GLLFLTLHTCLAHDPDSLRGHP---HSHGTHPCYSAEELPLGOAPP-HL-----LA----- 53

Db 44 GVFFYLTWSTFFLGGHVSNFLFHSQDYNNHSSPLSFSSADLSVASFHLNLTAFWK 103

QY 54 RGAK-----WG-----QALPVALV-----SSLEAAASHRGRHER 81

Db 104 RGSREVFSPKIQVFWDLDSKAKFDGSGSEPRSGFVIIVVDGEMGLLVGDSVKVAYARAKSAK 163

QY 82 PSATTQCPVLRPEEVLLEADTHORSISPWRYRYVDTDEDTPQKLAFAECLRCGIDAR---- 138

Db 164 PPTNFQALLLRKEHVFGA-----RVFTTKAREFGGKNREITSIDCRVDEDAKLCF 211

QY 139 -----TGRETAALNSVRLQSLV---LRRPCSRDGGSLPTPGAFAP 178

Db 212 SVDSKQVQLQIKLRWKFGRNEKVEIDGVHVQISWDVYNWLFQSKSGDGGGGGHVAFMF 271

QY 179 HTE 181

Db 272 RFE 274

RESULT 7

JL0032

hypothetical 31.7K protein (aphE region) - Streptomyces griseus

C:Species: Streptomyces griseus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Oct-1999

C:Accession: JL0032

R:Heinzel, P.; Werbitsky, O.; Distler, J.; Piepersberg, W.

Arch. Microbiol. 150, 184-192, 1988

A:Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep

A:Reference number: JL0031; MUID:88339496

A:Accession: JL0032

A:Molecule type: DNA

A:Residues: 1-297 <HEI>

A:Cross-references: GB:M37378; GB:X56876; NID:gl53162; PIDN:AAA26701.1; PID:gl53164

A:Experimental source: strain N2-3-11

A:Note: the function of the protein is unknown; the orf1 gene and aphE (streptomycies-3-

C:Genetics:

A:Gene: orf1

C:Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphE region)

Query Match

Best Local Similarity 8.0%; Score 86; DB 2; Length 297;

Matches 40; Conservative 15; Mismatches 55; Indels 36; Gaps 7;

QY 48 PPHLLARGAKWGOALPVAL-----VSSLEAAASH-----RGRHERPSA-----TTQ 87

Db 28 PSRLLLLG---WNRAPLVLDQLRSTARSTGSSVEVWADSAVPGPRGTEDRQAGRDVRFQ 85

QY 88 CPVLRPEEVLLEADTHORS-----ISPMRYRVDTDEDTPQKLAFAECLRCGIDARTGRET 143

Db 86 APLSRPETLLGLDLDRYDAVVVLGPDR---GDGPHDPDDMTLVALLAVLLDGRGTRET 141

QY 144 AALNSVRLQLSLVLRRLRRCSDRGSG 169

Db 142 -----RVVTVELVDDRRRLAPVNSG 161

RESULT 8

A42091

transcription activator SNF2/SWI2 homolog brm - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999

C:Accession: A42091

R:Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, T

Cell 68, 561-572, 1992

A:Title: brahma: a regulator of Drosophila homeotic genes structurally related to the

A:Reference number: A42091; MUID:92154670

A:Accession: A42091

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1638 <TAM>

A:Cross-references: GB:M85049; NID:gl57011; PIDN:AAA19661.1; PID:gl57012

A:Experimental source: iso-1

A:Note: sequence extracted from NCBI backbone (NCBIN:82354, NCBIP:82360)

C:Genetics:

A:Gene: FlyBase:brm

A:Cross-references: FlyBase:FBgn0000212

A:Superfamily: unassigned bromodomain proteins; bromodomain homology

C:Keywords: transcription regulation

F:1451-1506/Domain: bromodomain homology <BRO>

Query Match 7.9%; Score 84.5; DB 2; Length 1638;

Best Local Similarity 22.2%; Pred No. 17;

Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;

QY 22 PSLRGHPHSHGTHPCYSAEELPLGOAPP-H---LLARGAKWGOALPVALVSSLEAAASHRG 77

Db 52 PGAYGHPMQHGPP---GQGGPHHMPHHQGMFISKPGHGMQMB---PTGNMSPYQT 104

QY 78 RHERPSATTQCPVLR-----PEEVLLEADTH---QRSISPWRYRVDTDEDTPQKLA 125

Db 105 HGMPNPAPTQPCIVSPGGPPGPPPPERSQENLHALQRAIDSMEEKGLQEDPRYSOLLA 164

QY 126 FAECLRCGIDARTGRTAALNSVRLQSL-----LLVLRRLRRCPSRD----- 166

Db 165 -----WRATSKHOHLNGVQLNLLRTQITAYRLLRNKKPISMQMQLQAQAOQPPPP 215

QY 167 GSGLPTPGA 175

Db 216 GPPIGPPGA 224

RESULT 9

S76371

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S76371

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S76371

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <KAN>
A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10223.1; PID:g100159
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: gida protein

Query Match 7.7%; Score 82.5; DB 2; Length 635;
Best Local Similarity 24.2%; Pred. No. 9.2;
Matches 44; Conservative 21; Mismatches 60; Indels 57; Gaps 8;

QY 19 HHPSLRGHPHSGTTPHCYSAEEL-----PLGQAPPHLLARGAKWG--QA 61
Db HLSPIYGFIDSKGPRYCPSTQKIVRFADKESHQIFIEPEGRDIPELYIQGFSTGLPEN 326
QY 62 LPVALVSSLEAASHRGHERPSATTQCPVLRPEEVLADTHQRSISPWRYVDTDEDRYP 121
Db VOLAMLTLPGLN-----CVMLRPAYAVEYDFLPAT-----QCYP 362
QY 122 OKLA--FAECLCRGCI DARTGRETAA-----LNSVRLQ--SLLVLRRRPCSRDGSGL 170
Db SLMTKKVAGLFCAGQINGTTGYEENAAQGLVAGINARHCQKSLIIF-----SREGSYL 417
QY 171 PT 172
Db 418 GT 419

RESULT 10
T23218
hypothetical protein K02B12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C:Accession: T23218
R:Harris, B.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19710
A:Accession: T23218
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-325 <WIL>
A:Cross-references: EMBL:Z75711; PIDN:CAB00031.1; GSPDB:GN000019; CESP:K02B12.1
A:Experimental source: clone K02B12
C:Genetics:
A:Gene: CESP:K02B12.1
A:Map position: 1
A:Introns: 155/2; 189/3; 234/3; 268/3
C:Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 7.6%; Score 81.5; DB 2; Length 325;
Best Local Similarity 25.9%; Pred. No. 5.5;
Matches 29; Conservative 14; Mismatches 54; Indels 15; Gaps 4;

QY 9 FLFWLHTLAHDPSSLRGHPHSGTTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVS 68
Db FQDPHTPMLYQPOLHFMFLPQHDWAYPHLAQSLP---PPHLTPS-----TAAVA 59
QY 69 SLEAASHRGHERPSATTQCPVLR-PEEVLADTHQRSISPW--RYRVDTDE 117
Db AATIASQSSIINOTSIVTSTPSCQIKQEVERPEIIQRLMPPPPAYQFSCDD 111

RESULT 11
D83640
hypothetical protein PA0049 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83640
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Miziochuchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.K.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: D83640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-553 <STO>
A:Cross-references: GB:AE004444; GB:AE004091; NID:g9945863; PIDN:AAG03439.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0049

Query Match 7.5%; Score 81; DB 2; Length 553;
Best Local Similarity 24.2%; Pred. No. 11;
Matches 55; Conservative 16; Mismatches 72; Indels 84; Gaps 13;

QY 12 WLHTCLAHDPSSLRGHPHSGTTPHCYSAEEL-----LGOAPPHLLARG----- 55
Db 305 WLEAWNGRFGSSAG---NDGIVCPADSPALPNVPLPGSVTNPGTAPISLRGSGCINP 361
QY 56 -----AKGQALPVALVS-----LEAASHRGHERPSATTQCPVLRPEEVL 98
Db 362 PRWLGYDSASRWRONLPQAQFSKASLPVRLLAADTWRTGIERPPGATSA-----AEGFD 416
QY 99 ADTHQRSISPWRYVDTDEDRYPQKLAFAECLCRGCI DARTGRETALNSV--RLQSL 156
Db 417 VTWH-----TNYDFFD-----CANPT--ENVPTNGVMAMPDPSL 451

QY 157 VL--RRRPPCSRDGSG--LPTPGAF-----AFHTEF-----IHVPV 187
Db 452 VLPNRRICARNGGGDYLSNESAYRTVLRDAFRLIIPAGHIHVPV 498

RESULT 12
B40203
4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Mar-2000
C:Accession: B40203
R:Yang, B.Z.; Ding, J.H.; Enghild, J.J.; Bao, Y.; Chen, Y.T.
J. Biol. Chem. 267, 9294-9299, 1992
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle glyc
C:Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase
A:Reference number: A40203; MUID:92250533
A:Accession: B40203
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-210 <YAN>
C:Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysacc

Query Match 7.5%; Score 80.5; DB 2; Length 210;
Best Local Similarity 25.3%; Pred. No. 4.2;
Matches 50; Conservative 17; Mismatches 76; Indels 55; Gaps 10;

QY 22 PSLRGHPHSGT--PHCYS-AEELPLG---QAPPHLLARGAKWGQALPVALVSSLEAAASH 75
Db 3 PTLQGPVTYVYTWPCYSIADQLELNPDFSPPK-----KEWNMLCIDVTVTNHTAANS 57
QY 76 RGRHERPSAT-----TQCPVLRPEEVL---LEADTHQRSISPWRYRVDTDE 118
Db 58 RWLHEHPECAYNLVNSPHHKALWHLSCDVAEGRGVFALIENDHMSI-----RLIWE 112
QY 119 RYPQKLAFAECLCRGCI DARTGRETALNSVRLQSLVLRRRPCSRDGSGLTTP----- 173
Db 113 IFPEKLIQMGDQVKQAYDA-----LPSSTIV--SMACCASGSKWNPAAPS 157
QY 174 --GAFAPHTEFIHVPVGC 189
Db 158 DTGEVNFQSGIIEVPQVC 175

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Query Match          7.4%; Score 79.5; DB 2; Length 638;
Best Local Similarity 30.3%; Pred. No. 18;
Matches 36; Conservative 10; Mismatches 56; Indels 17; Gaps 6;
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Search completed: August 23, 2002, 16:02:16
Job time: 82 sec

Search completed: August 23, 2002, 16:02:16
Job time: 82 sec

Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	173	16.1	153	1	US-08-514-014-12	Sequence 12, Appl	
2	173	16.1	153	2	US-08-833-823-12	Sequence 12, Appl	
3	173	16.1	163	3	US-09-034-810-2	Sequence 2, Appl	
4	173	16.1	163	3	US-08-685-239-2	Sequence 2, Appl	
5	160.5	15.0	151	2	US-08-620-694A-8	Sequence 8, Appl	
6	160.5	15.0	151	3	US-09-034-810-6	Sequence 6, Appl	
7	160.5	15.0	151	3	US-09-022-255-8	Sequence 8, Appl	
8	160.5	15.0	151	3	US-09-022-696-8	Sequence 8, Appl	
9	160.5	15.0	151	3	US-08-685-239-6	Sequence 6, Appl	
10	160.5	15.0	151	3	US-09-022-253-8	Sequence 8, Appl	
11	160.5	15.0	151	3	US-09-022-260-8	Sequence 8, Appl	
12	160.5	15.0	151	4	US-09-022-259-8	Sequence 8, Appl	
13	160.5	15.0	151	4	US-09-022-257-8	Sequence 8, Appl	
14	160.5	15.0	151	4	US-08-432-994A-8	Sequence 8, Appl	
15	158	14.7	155	4	US-08-432-994A-4	Sequence 8, Appl	
16	150.5	14.0	158	2	US-08-620-694A-7	Sequence 7, Appl	
17	150.5	14.0	158	3	US-09-022-255-7	Sequence 7, Appl	
18	150.5	14.0	158	3	US-09-022-696-7	Sequence 7, Appl	
19	150.5	14.0	158	3	US-09-022-253-7	Sequence 7, Appl	
20	150.5	14.0	158	3	US-09-022-260-7	Sequence 7, Appl	
21	150.5	14.0	158	4	US-09-022-259-7	Sequence 7, Appl	
22	150.5	14.0	158	4	US-09-022-257-7	Sequence 7, Appl	
23	148.5	13.8	150	3	US-09-034-810-4	Sequence 4, Appl	
24	148.5	13.8	150	3	US-08-685-239-4	Sequence 4, Appl	
25	148.5	13.8	150	4	US-08-432-994A-2	Sequence 2, Appl	
26	148.5	13.8	158	4	US-08-432-994A-10	Sequence 10, Appl	
27	125	11.6	179	4	US-08-432-994A-6	Sequence 6, Appl	

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Db 60 MSRNIESRSTSPWNYTVTWDPNRYPSVVOAQCRLGGINAQ-GKEDISMNSVPIQOETL 118
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCVP 194
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVP 147

RESULT 2
US-08-833-823-12
; Sequence 12, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-823-12

Query Match 16.1%; Score 173; DB 2; Length 153;
Best Local Similarity 39.0%; Pred. No. 9.4e-13;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPWRYVDTEDEDRYPQKLAFAECLRCGIDARTGRTAALNSVRLQSL 156
Db 60 MSRNIESRSTSPWNYTVTWDPNRYPSVVOAQCRLGGINAQ-GKEDISMNSVPIQOETL 118
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCVP 194
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVP 147

RESULT 3
US-09-034-810-2
; Sequence 2, Application US/09034810
; Patent No. 6043344
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
```

```
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden'Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,239
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-034-810-2

Query Match 16.1%; Score 173; DB 3; Length 163;
Best Local Similarity 39.0%; Pred. No. 1e-12;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPWRYVDTEDEDRYPQKLAFAECLRCGIDARTGRTAALNSVRLQSL 156
Db 70 MSRNIESRSTSPWNYTVTWDPNRYPSVVOAQCRLGGINAQ-GKEDISMNSVPIQOETL 128
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCVP 194
Db 129 VVRKHQGC-----VSFQLEKVLVTGCTCVP 157

RESULT 4
US-08-685-239-2
; Sequence 2, Application US/08685239
; Patent No. 6074849
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden'Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
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NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,239
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: G15262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 163 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-685-239-2

	Query Match	16.1%; Score 173; DB 3;	Length 163;
	Best Local Similarity	39.0%; Pred. No. le-12;	
	Matches 39; Conservative	16; Mismatches 31;	Indels 14; Gaps 3;
QY	97 LEADTHORISPNRYVDTDEDRYPOKLAFACLCRCIDARTGRTAALNSVRLLQSLL	156	
DB	70 MSRIEKRSTSPNNVTYTFDNPFRSEVVQAQCRLGCINAAQ-KGEDISMNSVPTIQETL	128	
QY	157 VLRRR--PCSRDGSLGTPTGAFATFHFIHPVGCTCPLP	194	
DB	129 VRRKHOGCS-----VSFOLEKLVTVGCTCVTP	157	

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RESULT      5
US-8-620-694A-8
: Sequence 8, Application US/08620694A
: Patent No. 5859286
: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Apple, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/620,694A
: FILING DATE: 21 MARCH 1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:

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APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-08-620-694A-8

Query Match	15.0%;	Score 160.5;	DB 2;	Length 151;
Best Local Similarity	28.6%;	Prod. No. 2.8e-11;		
Matches	46;	Conservative 23;	Mismatches 57;	Indels 35; Gaps 5;
Qy	36	CYSAEELPLGQAPHILLARGAKWQCALPVALVLSLEAAASHRGHERPSAATQCPVLREE	95	
Db	18	CIVKSEITSAQTPCLAA-----NSNPSRYMVMTLSIRNWNMTSSKRAS-----	60	
Qy	96	VLEADTHORSTPWRYRVDTDEDYRYPKLAFAECLGCGCIDARTGRTAALNSVRLQLSL	155	
Db	61	---DYNNRSTSPWTLIHNEQDDRYPSVINEFAKCRYLCGVNA-DCNVVDYHMNSVPIQOEI	115	
Qy	156	LVLRR--RPCRSDSGSLPTPGAFATHEFIHVPVGCTCVLP	194	
Db	116	LAVRKGHQPCPN-----SFRLEKMI-VTVGCTCVTP	145	

RESULT 6
US-09-034-810-6
Sequence 6, Application US/09034810
Patent No. 6043344
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
APPLICANT: Goldman, Samuel
APPLICANT: Pittman, Debra
APPLICANT: Mi, Sha
APPLICANT: Neben, Steven
APPLICANT: Giannotti, JoAnn
APPLICANT: Golden/Fleet, Margaret
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/034,810
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: 08/685,239
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brown, Scott A.
;; REGISTRATION NUMBER: 32,724
;; REFERENCE/DOCKET NUMBER: G15/62
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8224
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 151 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-034-810-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRHPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSPFRSVVMVTLIRNWTSSKRAS----- 60

QY 96 VLEADTHQRSIPWRYRVDTEDEYPOKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMSVPIQOEI 115

QY 156 LVLR--RPCSRDGLPTPGAFATHTFTHVPVGCTCVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCVTP 145

RESULT 7
US-09-022-255-8
; Sequence 8, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: USSN 08/410,535
;; FILING DATE: 23 MARCH 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,695
;; REFERENCE/DOCKET NUMBER: 2617-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 151 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Herpesvirus Saimiri
;; STRAIN: ORF13
US-09-022-255-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRHPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSPFRSVVMVTLIRNWTSSKRAS----- 60

QY 96 VLEADTHQRSIPWRYRVDTEDEYPOKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMSVPIQOEI 115

QY 156 LVLR--RPCSRDGLPTPGAFATHTFTHVPVGCTCVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCVTP 145

RESULT 8
US-09-022-696-8
; Sequence 8, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535

; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVVALVSSLEAASHRGHRHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHQRSISPRWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRTAALNSVRLLOSL 155
Db 61 ----DYNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMNSVPIQQEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHEFIHVPVGTCTVLP 194
Db 116 LVVRKGHPCPN-----SFRLEKMLTVGTCTVTP 145

RESULT 9
US-08-685-239-6
; Sequence 6, Application US/08685239
; Patent No. 6074849
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,239
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-685-239-6
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVVALVSSLEAASHRGHRHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHQRSISPRWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRTAALNSVRLLOSL 155
Db 61 ----DYNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMNSVPIQQEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHEFIHVPVGTCTVLP 194
Db 116 LVVRKGHPCPN-----SFRLEKMLTVGTCTVTP 145
RESULT 10
US-09-022-253-8
; Sequence 8, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 6096305 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-253-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVVMVTLIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPWRYRVDTDEDPYQKLAFAECLRCGICDARTGRTAALNSVRLQLSL 155
Db 61 ----DIYNRSTSPWTLHRNEDQDRPYSVIWEAKCRYLGCVNA-DGNVDYHMSNPVPIQOEI 115
QY 156 LVLR--RPCSRDGSGLPTPGAFATFETHVPVGCTCVLP 194
Db 116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145

RESULT 11
US-09-022-260-8
; Sequence 8, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-260-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVVMVTLIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPWRYRVDTDEDPYQKLAFAECLRCGICDARTGRTAALNSVRLQLSL 155
Db 61 ----DIYNRSTSPWTLHRNEDQDRPYSVIWEAKCRYLGCVNA-DGNVDYHMSNPVPIQOEI 115
QY 156 LVLR--RPCSRDGSGLPTPGAFATFETHVPVGCTCVLP 194
Db 116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145

RESULT 12
US-09-022-259-8
; Sequence 8, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-259-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHERPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRTAALNSVRLQSL 155
DB 61 ----DYNNSTSPWTLHRNEDQDRPSVWEAKCRVLGCVNA-DGNVDYHMSVPIQOEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHTFIHVPVGCCTVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVP 145

RESULT 13
US-09-022-257-8
Sequence 8, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-257-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHERPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRTAALNSVRLQSL 155
DB 61 ----DYNNSTSPWTLHRNEDQDRPSVWEAKCRVLGCVNA-DGNVDYHMSVPIQOEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHTFIHVPVGCCTVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVP 145

RESULT 14
US-08-432-994A-4
Sequence 4, Application US/08432994A
Patent No. 6274711
GENERAL INFORMATION:
APPLICANT: Golstein, Pierre
APPLICANT: Rouvier, Eric
APPLICANT: Fossiez, Francois
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Djossou, Odile
APPLICANT: Banchem, Jacques
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,994A
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/250,846
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,747
FILING DATE: 05-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,203

```

;
; ATTORNEY/AGENT INFORMATION:
;
;   NAME: Ching, Edwin P.
;
;   REGISTRATION NUMBER: 34, 090
;
;   REFERENCE/DOCKET NUMBER: DX0388K3
;
; TELECOMMUNICATION INFORMATION:
;
;   TELEPHONE: 415-852-9196
;
;   TELEFAX: 415-496-1200
;
;   INFORMATION FOR SEQ ID NO: 8:
;
;     SEQUENCE CHARACTERISTICS:
;
;       LENGTH: 155 amino acids
;
;       TYPE: amino acid
;
;       TOPOLOGY: linear
;
;     MOLECULE TYPE: protein
;
; US-08-432-994A-8

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	Query Match	14.7%;	Score 158;	DB 4;	Length 155;
	Best Local Similarity	39.8%;	Pred. No. 5.7e-11;		
	Matches	39;	Conservative	11;	Mismatches 34; Indels 14; Gaps 3;
QY	99	ADTHQRSISPWRYVDTDEDRYPQKLAFAECLRGCCIDARTGRETAAALNSVRLLQSLLVL	158		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Db	64	SDYNRSTSPWNLHRNEDPERPSPVWEAKCRHLGCINA-DGNVDVHMNSVP IQQEILVL	122		
QY	159	RRRP--CSRDSGLTPGAFAHTEFHVPGCTCVLP	194		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Db	123	RRPPHCNP-----SFRLEKILVSGVGTCTVTP	149		

Search completed: August 23, 2002, 16:01:11
Job time: 22 sec

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RESULT 15
US-08-432-994A-8
; Sequence 8, Application US/08432994A
; Patent No. 6274711
; GENERAL INFORMATION:
; APPLICANT: Golstein, Pierre
; APPLICANT: Rouvier, Eric
; APPLICANT: Fossiez, Francois
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Djossou, Odile
; APPLICANT: Banchereau, Jacques
; TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432.994A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/250,846
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,747
; FILING DATE: 05-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,203
; FILING DATE: 14-JUN-1993

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